

## SEQUENCE LISTING

<110> Genentech, Inc.  
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<120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

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<140> 09/665,350  
<141> 2000-09-18

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<212> PRT  
<213> Homo sapiens

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1 5 10 15

Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His  
20 25 30

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr  
35 40 45

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr  
 50 55 60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu  
65 70 75 80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala  
85 90 95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr  
 100 105 110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys  
115 120 125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser  
130 135 140

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
 145 150 155 160

Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
 165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
 180 185 190

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
 195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
 210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
 225 230 235 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
 245 250 255

Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
 260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
 275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
 290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
 305 310 315 320

Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala  
 325 330 335

Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp  
 340 345 350

Leu

<210> 3

<211> 2206

<212> DNA

<213> Homo sapiens

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 aacagccctg gctgaggagg ctgcagcgca gcagagtatac tgacggcgcc aggttgccta 180  
 ggtgcggcac gaggagttt cccggcagcg aggaggctt gagcagcatg gcccggagga 240

<210> 4  
<211> 379

<212> PRT  
<213> *Homo sapiens*

<400> 4

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser  
1 5 10 15

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln  
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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

65	70	75	80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln			
85		90	95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly			
100		105	110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro			
115		120	125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln			
130	135	140	
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu			
145	150	155	160
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
165		170	175
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys			
180		185	190
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His			
195		200	205
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys			
210		215	220
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn			
225	230	235	240
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys			
245		250	255
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln			
260		265	270
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys			
275		280	285
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu			
290		295	300
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys			
305		310	315
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His			
325		330	335
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala			
340		345	350

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu  
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp  
 370 375

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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<212> DNA  
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<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 6  
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 7  
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<210> 8  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 8  
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<210> 9  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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22

<210> 10  
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 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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23

<210> 11  
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<212> PRT

<213> Homo sapiens

<400> 12

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20 25 30

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys  
35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu  
50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
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Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro  
85 90 95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr  
100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln  
                   115                  120                  125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln  
 130 135 140

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly  
145 150 155 160

His Asp Pro Gly

<210> 13  
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<212> DNA  
<213> Homo sapiens

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<222> (80)  
<223> a, t, c or g

<220>  
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<222> (94)  
<223> a, t, c or g

<220>  
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<222> (144)  
<223> a, t, c or g

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<223> a, t, c or g

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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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Pro	Pro	Ser	Leu	Arg	Cys	Ser	Leu	His	Ser	Ala	Cys	Cys	Ser	Gly	Asp
															45

Pro	Ala	Ser	Tyr	Arg	Leu	Trp	Gly	Ala	Pro	Leu	Gln	Pro	Thr	Leu	Gly

Val	Val	Pro	Gln	Ala	Ser	Val	Pro	Leu	Leu	Thr	Asp	Leu	Ala	Gln	Trp
65															80

Glu	Pro	Val	Leu	Val	Pro	Glu	Ala	His	Pro	Asn	Ala	Ser	Leu	Thr	Met
															95

Tyr	Val	Cys	Thr	Pro	Val	Pro	His	Pro	Asp	Pro	Pro	Met	Ala	Leu	Ser
															110

Arg	Thr	Pro	Thr	Arg	Gln	Ile	Ser	Ser	Ser	Asp	Thr	Asp	Pro	Pro	Ala
															125

Asp	Gly	Pro	Ser	Asn	Pro	Leu	Cys	Cys	Cys	Phe	His	Gly	Pro	Ala	Phe
130															140

Ser	Thr	Leu	Asn	Pro	Val	Leu	Arg	His	Leu	Phe	Pro	Gln	Glu	Ala	Phe
145															160

Pro	Ala	His	Pro	Ile	Tyr	Asp	Leu	Ser	Gln	Val	Trp	Ser	Val	Val	Ser
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Pro	Ala	Pro	Ser	Arg	Gly	Gln	Ala	Leu	Arg	Arg	Ala	Gln			

&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctcctgcaaa gccc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20

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24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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 gaccgaccag ctgagcaggc ggcagatccg cgagtagccaa ctctacagca ggaccagtgg 180  
 caagcacgtg caggtcaccg ggcgtcgcata ctccgcacc gccgaggacg gcaacaagtt 240  
 tgccaagctc atatgtggaga cggacacggtt tggcagccgg gttcgcata aaggggctga 300  
 gagtgagaag tacatctgtta tgaacaagag gggcaagctc atcgggaagc ccagcgggaa 360  
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 cgccccggcac gagggtctggt tcataggcatt cacgcggcag gggggcccccc gccaggcttc 480  
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 ccccaaaaaaaa ccaaactccctc ctggctagac tgttaggaagg gacttttggt tgggggggg 1080  
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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23  
 Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
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Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
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Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 24

cagtagtga gggaccaggg cgccatga

28

&lt;210&gt; 25

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 25
ccgggtgacct gcacgtgc tt gcca                                24

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<220>
<221> modified_base
<222> (21)
<223> a, t, c or g

<400> 26
gcggatctgc cgcctgctca nctggtcggt catggcgccc t                                41

<210> 27
<211> 2479
<212> DNA
<213> Homo sapiens

<400> 27
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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe  
65 70 75 80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140

Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160

Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175

Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190

Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205

Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220

Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240

Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255

Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270

Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285

Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300

Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320

Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335

Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350

Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Pro Gly Leu Pro  
 355 360 365

Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380

Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400

Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405	410	415
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val		
420	425	430
Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met		
435	440	445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly		
450	455	460
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu		
465	470	475
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu		
485	490	495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala		
500	505	510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser		
515	520	525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala		
530	535	540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser		
545	550	555
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys		
565	570	575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly		
580	585	590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln		
595	600	605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu		
610	615	620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His		
625	630	635
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu		
645	650	655
His Cys His Thr		
660		
<210> 29		
<211> 21		
<212> DNA		

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 29
cggtctacct gtatggcaac c                                21

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 30
gcaggacaac cagataaaacc ac                                22

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 31
acgcagattt gagaaggctg tc                                22

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 32
ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac    46

<210> 33
<211> 3449
<212> DNA
<213> Homo sapiens

<400> 33
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cgccctccac gagcgatccc cgaggagagc cgccggccctc ggcgaggcga agaggccogac 120

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ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatata 3360  
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 ttatacaata taaaattca ccacttcag 3449

<210> 34  
 <211> 915  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
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 Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile  
 20 25 30  
 Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45  
 Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
 50 55 60  
 Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
 65 70 75 80  
 Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
 85 90 95  
 Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
 100 105 110  
 Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
 115 120 125  
 His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
 130 135 140  
 Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
 145 150 155 160  
 Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
 165 170 175  
 Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
 180 185 190  
 Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
 195 200 205  
 Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
 210 215 220  
 Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225	230	235	240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile			
245		250	255
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser			
260	265		270
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
275	280		285
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
290	295		300
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
305	310	315	320
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
325		330	335
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
340	345		350
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
355	360		365
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
370	375		380
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys			
385	390	395	400
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
405	410		415
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420	425		430
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
435	440		445
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser			
450	455	460	
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465	470	475	480
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485	490		495
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
500	505		510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
 515 520 525  
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540  
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560  
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575  
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
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 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
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 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
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 625 630 635 640  
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
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 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670  
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685  
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
 690 695 700  
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
 705 710 715 720  
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
 725 730 735  
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
 740 745 750  
 Val Gly Lys Ala Ile Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765  
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
 770 775 780  
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
 805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
 820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
 835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
 850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
 865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
 885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
 900 905 910

Arg Tyr Arg  
 915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 36

acagccatgg tctatacggtt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 37  
 gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag 45  
  
 <210> 38  
 <211> 1813  
 <212> DNA  
 <213> Homo sapiens  
  
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 tttgtatgaa aaa 1813  
  
 <210> 39  
 <211> 390  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 39  
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20		25	30
Leu His Leu Pro Ala Asn Arg		Leu Gln Ala Val Glu Gly	Gly Glu Val
35		40	45
Val Leu Pro Ala Trp Tyr Thr	Leu His Gly Glu Val Ser Ser Ser Gln		
50	55	60	
Pro Trp Glu Val Pro Phe Val Met Trp Phe	Phe Lys Gln Lys Glu Lys		
65	70	75	80
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly	Val Thr Thr Ser Lys Pro		
85	90	95	
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn	Leu Ser Leu Arg		
100	105	110	
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly	Pro Tyr Ser Cys Ser Val		
115	120	125	
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly	His Ser Ile Lys Thr		
130	135	140	
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro	Pro Ser Cys Arg Leu		
145	150	155	160
Gln Gly Val Pro His Val Gly Ala Asn Val Thr	Leu Ser Cys Gln Ser		
165	170	175	
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln	Trp Asp Arg Gln Leu Pro		
180	185	190	
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp	Val Ile Arg Gly Ser		
195	200	205	
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala	Gly Val Tyr Val Cys		
210	215	220	
Lys Ala His Asn Glu Val Gly Thr Ala Gln	Cys Asn Val Thr Leu Glu		
225	230	235	240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala	Gly Ala Val Val Gly		
245	250	255	
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly	Leu Val Leu Leu Tyr His		
260	265	270	
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn	Asp Ile Lys Glu Asp		
275	280	285	

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
370 375 380

Gln Ala Gly Ser Leu Val  
385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> De

oligonucleotide probe

agggtctc

1955-1961 55 5

22

<211> 24

<212> DN

<213> Art

<213> Artificial sequence

52233

(22) Description of artificial sequence: synthetic oligonucleotide probe

400

41

attatggg

atggggggcc cggcagacat agac

24

210 42

<211> 50

<212> DNA

<213> Artificial sequence

1223

<<223> Description of Artificial  
oligonucleotide probe

<400> 42		
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc		50
<210> 43		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 43		
gtgtacaca gcgtggc		18
<210> 44		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 44		
gaccggcagg cttctgcg		18
<210> 45		
<211> 25		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 45		
cagcagcttc agccaccagg agtgg		25
<210> 46		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 46		
ctgagccgtg ggctgcagtc tcgc		24
<210> 47		





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Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val		
195	200	205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys		
210	215	220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe		
225	230	235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		
245	250	255
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		
260	265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		
275	280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		
290	295	300
Ile Gly Pro Leu Leu Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		
305	310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile		
325	330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		
340	345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		
355	360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		
370	375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		
385	390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		
405	410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		
420	425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		
435	440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		
450	455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
 465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu  
 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe  
 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val  
 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly  
 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile  
 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu  
 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His  
 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys  
 675 680 685

Leu Arg  
 690

<210> 50  
 <211> 589  
 <212> DNA  
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<220>  
 <221> modified\_base  
 <222> (61)

<223> a, t, c or g

<400> 50

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 gtattggtcc ct当地gcttc atcatctgac aacttcttat tgaaacctca aaattatgat 180  
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 gataggtata ggagtctatg tggcatttg gaatactcac ctgataaccat gaatggcagc 360  
 tggttttcag agggctgtga gctgacatac tcaaattgaga cccacacctc atgccgctgt 420  
 aatcacctga cacatttgc aattttgatg tcctctgtc cttccattgg tattaaagat 480  
 tataatattc ttacaaggat cactcaacta ggaataatta tttcaactgat ttgtcttgcc 540  
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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 52

ggagtagaaa gcgcattgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 54		
cgagctcgaa ttaattcg		18
<210> 55		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 55		
ggatctcctg agtcagg		18
<210> 56		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 56		
cctagttgag tgatccttgt aag		23
<210> 57		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
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atgagaccca cacctcatgc cgctgtataatc acctgacaca ttttgcaatt		50
<210> 58		
<211> 2137		
<212> DNA		
<213> Homo sapiens		
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ggacaagaa gccggccgct gcctgccccgg gcccggggag ggggttgggg ctggggccgg 180  
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ccatcccaac cggcactca cagccccgca ggcattcccg gtcggccccc agcctccgc 420  
accccatcg cggagctgc gccgagagcc ccagggaggt gccatcgaga gccccgtgt 480  
ggtgttccac gtatggatcc tggccggct ctggctggcc gtggccggc gccccctcgc 540  
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atttgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagaccta 1980  
gaacccttcc cccagcactt gttttccaa catgatattt atgagaattt tattttgata 2040  
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qaggttgggtt ttgtatatta aatggagtt tgtttgt 2137

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu  
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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65                   70                   75                   80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85                   90                   95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100               105               110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115               120               125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130               135               140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145               150               155               160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165               170               175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180               185               190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195               200               205

Val Arg Ser Pro Ser Phe Glu Lys  
 210               215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 60

atccgccccag atggctacaa tgtgtta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 61

gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta

42

<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 62  
 ccagtccggc gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
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 gctgtcgtc cgctacctgg tggtcgccct gggctatcat aaggcctatg ggtttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctattt tagcctgcaa 240  
 aaccccaaag aagactgttt cctccagatt agagtggaaag aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctctcaagg tgattttaaa aatcgagctg agatgataga 360  
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 acccggggagg cggaggttgc agtgagctga gatcacgcca ctgcagtcgc gcctggtaa 1200  
 cagagcaaga ttcacatctca aaaaataaaaa taaaataata aataaaatact ggTTtttacc 1260  
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<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
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 1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30



Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
                   35                                40                          45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
       50                          55                            60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
       65                          70                          75                  80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
       85                          90                          95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
       100                          105                          110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
       115                          120                          125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
       130                          135                          140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
       145                          150                          155                  160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
       165                          170                          175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
       180                          185                          190

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
       195                          200                          205

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
       210                          215                          220

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
       225                          230                          235                  240

Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
       245                          250                          255

Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
       260                          265                          270

Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
       275                          280                          285

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
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Gly Gly Ser Arg Gly Gln Glu Phe

305 310

<210> 65  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 65 atcgttgtga agttagtgcc cc 22

<210> 66  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 66 acctgcgata tccaacagaa ttg 23

<210> 67  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 67 ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

<210> 68  
<211> 2639  
<212> DNA  
<213> Homo sapiens

<400> 68 gacatcgag gtgggctagc actgaaaactg ctttcaaga cgaggaagag gaggagaaaag 60 agaaaagaaga ggaagatgtt gggcaacatt tatttaacat gctccacagc ccggaccctg 120 gcatcatgct gctattcctg caaatactga agaagcatgg gattaaata ttttacttct 180 aaataaatga attactcaat ctcctatgac catctataca tactccacct tcaaaaaagta 240 catcaatatt atatcattaa ggaatatgta accttctt ctccaatatg catgacattt 300 ttggacaatg caatttgtgc actggactt atttcagtga agaaaaactt tgtggttcta 360 tggcattcat catttgacaa atgcaagcat cttccttatac aatcagctcc tattgaactt 420 actagcactg actgtggaat ccttaaggc ccattacatt tctgaagaag aaagctaaga 480 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagta 540

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gtgtgatatg tcttatcagc tgcctctc cagaaatgaa ctgtgatggt ggacacagct 2460  
atgtgaggaa ttacttacag aaaccaacct ttgcattagg tgagcttctt ctcctctga 2520  
taaatctctg ggaagcagga aaagaaaaaa gtacatcaact gaaagtaaaa gcaactgtt 2580  
taggtttacc aacaaatatg tcctaaaaac caccaggaa acctactcca aaaatgaac 2639

<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile  
1 5 10 15

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu  
20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
           35                        40                        45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
50 55 60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Gln Thr Asn Asn  
 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350	
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn			
355	360	365	
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr			
370	375	380	
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro			
385	390	395	400
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met			
405	410	415	
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu			
420	425	430	
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala			
435	440	445	
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu			
450	455	460	
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr			
465	470	475	480
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys			
485	490	495	
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys			
500	505	510	
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys			
515	520	525	
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser			
530	535	540	
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr			
545	550	555	560
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys			
565	570	575	
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys			
580	585	590	
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn			
595	600	605	
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn			
610	615	620	

Asn	Thr	Thr	Thr	Leu	Met	Ala	Cys	Leu	Gly	Gly	Leu	Leu	Gly	Ile	Ile
625					630					635					640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
               660                   665                   670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70  
<211> 1305  
<212> DNA  
<213> Homo sap

<400> 70  
gccccggact ggcgcaaggt gcccaagcaa ggaaagaaaat aatgaagaga cacatgtttt 60  
agctgcagcc tttgaaaca cgcaagaagg aaatcaatag tgtggacagg gctggacct 120  
ttaccacgct tttggagta gatgaggaat gggctcgta ttatgtcac attccagcat 180  
gaatctggta gacctgtggc taaccctgttc cctctccatg tgtctctcc tacaaagttt 240  
tgttcttatg atactgtgct ttcattctgc cagttatgtgt cccaaaggct gtctttgttc 300  
ttcctctggg gttttaaatg tcacctgttag caatgcaaattt ctcaaggaaa tacctagaga 360  
tcttcctcct gaaacagtct tactgtatct ggactccaaat cagatcacat ctattcccaa 420  
tgaatTTTT aaggacctcc atcaacttgag agttctcaac ctgtccaaaaa atggcatttt 480  
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttggc 540  
cgacaatcggtt attcaaagggt tgccaaaaaa tgccctcaat aacctgaagg ccaggccag 600  
aattgccaac aacccttggc actgcgactg tactctacag caagtctga ggagcatggc 660  
gtccaatcat gagacagccc acaacgttatg ctgtaaaacg tccgtgttgg atgaacatgc 720  
tggcagacca ttccctcaatg ctgccaacgca cgctgaccc ttgtacccctcc ctaaaaaaaac 780  
taccgattat gccatgtgg tcaccatgtt tggctggttc actatggta tctcatatgt 840  
ggtatattat gtgaggcaaa atcaggagga tgcccgaga cacctcgaaatc acttggaaatc 900  
cctgccaagc aggcagaaga aagcagatga acctgtatgat attagcactg tggatatgt 960  
tccaaactga ctgtcattga gaaagaaaaga aagttagttt cgattgcagt agaaataagt 1020  
ggtttacttc tcccatccat tgtaaaccatt tgaaactttt tatttcagtt tttttgaat 1080  
tatgccactg ctgaacttti aacaaacact acaacataaa taatttgagt ttaggtgatc 1140  
cacccttaa ttgtacccccc gatggtatat ttctgagttaa gctactatctt gaacattttt 1200  
tagatccatc tcactattta ataatgaaat ttatTTTTT aattttaaaag caaataaaaag 1260  
cttaactttt aaccatggga aaaaaaaaaaaa aaaaaaaaaaaa aaaca 1305

<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
 1 5 10 15

Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220

Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255

Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

accgagccga gcccggaccgaa ggccgcggccg agatgcaggt gagcaagagg atgctggcgg 60  
 gggggctgtgag gaggcatgcccc agccccatcc tggcctgtcg gcagccatc ctccctgtgg 120  
 tgctgggctc agtgcgtgtca ggctcgccca cgggctgccc gccccgtgc gagtgctccg 180  
 cccaggaccg cgctgtgtcg tgccacccgca agtgctttgt ggcagtcccc gagggcatcc 240  
 ccaccggagac gcccgtgtcg gacctaggca agaaccgcac caaaaacgcac aaccaggacg 300  
 agttcgccag cttcccgac acgtggaggac tggagctcaa cgagaacatc gtgagcgccg 360  
 tggagcccg cgccttcaac aaccttca acctccggac gctgggtctc cgcagcaacc 420  
 gcctgaagct catcccgcta ggcgttca ctggccttag caacctgacc aaggcaggaca 480  
 tcagcgagaa caagatcgat atcctactgg actacatgtt tcaggacctg tacaaccccta 540  
 agtcactgga gtttggcgac aatgacactcg tctacatctc tcacccgcgc ttcagcggcc 600  
 tcaacagccct ggagcagctg acgtggaga aatgcaaccc gacccatc cccaccggagg 660  
 cgctgtccca cctgcacccgac ctcatgtcc tgaggctccg gcacccataac atcaatgcca 720  
 tccgggacta ctccctcaag aggctgtacc gactcaaggt cttggagatc tcccactggc 780  
 cctacttgga caccatgaca cccaaactgac tctacggcct caacccgtacg tccctgtcca 840  
 tcacacactg caatctgacc gctgtgcct acctggccgt ccggccaccta gtctatctcc 900  
 gcttcctcaa cctctcttac aaccccatca gcaccattga gggtccatg ttgcattgagc 960  
 tgctccggct gcaggagatc cagctggtgg gcccggcagct ggcgtggtg gagccctatg 1020  
 cttcccgccg cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080  
 tggaggaatc agtcttccac tcgggtggca acctggagac actcatctcg gactccaacc 1140  
 cgctggctg cgactgtcg ctcctgtgg tggtccggc ccgtggcgct ctcaacttca 1200  
 accggcagca gcccacgtgc gccacgcccc agtttgtcca ggcaaggag ttcaaggact 1260  
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 aggcccagca ggtgtttgtg gacgaggggcc acacgggtca gtttgtgtc cgggcccgtg 1380  
 gcgaccggcc gcccggccatc ctctggctc caccggaaa gcacccgtgc tcagccaaga 1440  
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 aggacaacgg cacgtacccg tgcacccgcgg ccaacggggg cggcaacgcg tccatggccg 1560  
 cccacctgca tgtgcgcagc tactccggcc actggccca tcagccaaac aagaccttcg 1620  
 ctttcatctc caaccagccg ggcgaggggag aggccaaacag caccggccgc actgtgcctt 1680  
 tccccctcga catcaagacc ctcatcatcg ccaccacat gggcttcatc tcttcctgg 1740  
 gcgctgtcct ctctgcctg gtgtgtgtt ttctctggag ccggggcaag ggcaacacaaa 1800  
 agcacaacat cgagatcgag tatgtgcccc gaaagtccga cgcaggcatc agtccggccg 1860  
 acgcgccccg caagttcaac atgaagatga tatgaggccg ggggggggg cagggacccc 1920  
 cggggggccg ggcaggggaa gggccctggt cggccacccgc tcactctcca gtccttccca 1980  
 cctccctccct acccttctac acacgttctc ttctccctc ccggccctcg cccctgtgc 2040  
 ccccccggccag ccctcaccac ctggccctct tctaccagga cctcagaagc ccagacctgg 2100  
 ggacccccc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160  
 ggcagagtca ataattcaat aaaaaagttt cgaactttct ctgttaacttgc gtttcaata 2220  
 attatggatt tttatgaaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280  
 aaaaaaaaaa 2290

&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

1

5

10

15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
                   20                  25                  30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
                   35                  40                  45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
                   50                  55                  60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
                   65                  70                  75                  80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
                   85                  90                  95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
                   100                105                110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
                   115                120                125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
                   130                135                140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
                   145                150                155                160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
                   165                170                175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
                   180                185                190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
                   195                200                205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
                   210                215                220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
                   225                230                235                240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
                   245                250                255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
                   260                265                270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
                   275                280                285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
                   290                295                300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Ala Asn Ser Thr  
 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590
Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser		
595	600	605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile		
610	615	620

<210> 74  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<p>&lt;400&gt; 74</p>		22
tcacctggag cctttattgg cc		

<210> 75  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<p>&lt;400&gt; 75</p>		23
ataccagcta taaccaggct gcg		

<210> 76  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<p>&lt;400&gt; 76</p>		50
caacagtaag tggtttgatg ctcttccaaa tcttagagatt ctgtatgattg		
gg		52

<210> 77  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 77 ccatgtgtct cctcctacaa ag	22
<210> 78 <211> 23 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 78 gggaatagat gtgatctgat tgg	23
<210> 79 <211> 50 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 79 cacctgttagc aatgcaaatc tcaaggaaat acctagagat cttccctcctg	50
<210> 80 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 80 agcaaccgcc tgaagctcat cc	22
<210> 81 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 81 aaggcgccgt gaaaagatgt a gacg	24
<210> 82	

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcaactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 cccacgcgtc cgcacctcg ccccggtc cgaagcgct cggggcgcc cttdcggtca 60  
 acatcgtagt ccacccctc cccatccccca gccccccggg attcaggctc gccagcgccc 120  
 agccagggag cggccggga agcgcgtatgg gggcccccagc cgctcgctc ctgctctgc 180  
 tcctgctgtt cgccctgctgc tggcgcccg gcgccggccaa cctctcccaag gacgacagcc 240  
 agccctggac atctgtatgaa acagtggtgg ctggggcac cgtggtgctc aagtgc当地 300  
 tgaaaatca cgaggactca tccctgcaat ggtctaaccct tgctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctt acgccccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagttac acctgctcaa 480  
 tccttactat gcctgtgcga actgc当地 540  
 agcccatcat cactggttat aaatcttcat tacggaaaa agacacagcc accctaaact 600  
 gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaagggt gaccaagaac 660  
 tccacggaga accaaccgc atacaggaag atcccaatgg taaaacctt actgtcagca 720  
 gtcgggtgac attccaggtt accccgggagg atgatggggc gagcatctg tgctctgtga 780  
 accatgaatc tctaaaggga gctgacagat ccacctctca acgcattgaa gtttataaca 840  
 caccactgc gatgatttagg ccagaccctc cccatcccg tgagggccag aagctgttgc 900  
 tacactgtga gggtcgcggc aatccagttcc cccagcagta cctatggag aaggaggca 960  
 gtgtgccacc cctgaagatg acccaggaga gtgc当地 1020  
 gtgacagtgg cacctacggc tgcacagcca ccagcaacat gggcagctac aaggcctact 1080  
 acaccctcaa tgttaatgac cccagtc当地 1140  
 tc当地 1200  
 gcaactactt gatccggcac aaaggaacct acctgacaca tgaggcaaaa ggctccgacg 1260  
 atgctccaga cgcggacacg gccatcatca atgc当地 1320  
 acaagaagga atatttcatc tagagggcc tgcccaactt ctgc当地 1380  
 gtggggactg ctggggccgt caccacccg gacttgc当地 1440  
 ctcccgctt ctccccagcc caccaccc cctgtacaga atgtctgtt tgggtgc当地 1500  
 tttgtactcg gtttggaaatg gggagggagg agggc当地 1560  
 cccttccgt ggcttctgt catttgggtt attatttt ttgtacaaat cccaaatcaa 1620  
 atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa aacaaacaaa 1680  
 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Met Gly Ala Pro Ala Ser Leu Leu Leu Leu Leu Phe Ala  
 1 5 10 15

Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
 20 25 30

Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290                            295                            300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305                            310                            315                            320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325                            330                            335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340                            345                            350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355                            360                            365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
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Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
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<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

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22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

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22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

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<400> 87
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<210> 88
<211> 50
<212> DNA
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<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 88
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<210> 89
<211> 50
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

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<210> 90
<211> 2755
<212> DNA
<213> Homo sapiens

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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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                  20                 25                 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr  
 35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe  
50 55 60

Leu	His	Gly	Asn	Ser	Leu	Thr	Arg	Leu	Phe	Pro	Asn	Glu	Phe	Ala	Asn
65					70					75					80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu  
85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125

Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140

Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160

Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175

Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190

Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205

Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220

Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
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Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255

Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270

Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285

Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300

Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320

Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335

Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350

Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365

Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
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 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420                    425                    430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
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 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
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 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
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 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485                    490                    495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500                    505                    510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
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 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
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 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565                    570                    575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580                    585                    590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
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 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
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 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625                    630                    635                    640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
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 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

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Cys Gly Ser His Ser Leu Ser Asp		
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<211> 22		
<212> DNA		
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
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<210> 93		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 93		
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<210> 94		
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
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<210> 95		
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<213> Homo sapiens		
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<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

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      81          10         15

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50 55 60

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Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu			
85	90	95	
Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly			
100	105	110	
Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu			
115	120	125	
Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala			
130	135	140	
Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met			
145	150	155	160
Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu			
165	170	175	
Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr			
180	185	190	
Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro			
195	200	205	
Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val			
210	215	220	
Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly			
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245	250	255	
Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu			
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Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr			
275	280	285	
Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg			
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Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln			
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385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
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Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
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&lt;210&gt; 97

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 97

tggaaggaga tgcgtatgccca cctg

24

&lt;210&gt; 98

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 98

tgaccagtgg ggaaggacag

20

<210> 99  
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 <212> DNA  
 <213> Artificial Sequence

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<400> 99  
 acagagcaga gggtgccctg 20

<210> 100  
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 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 100  
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<210> 101  
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 <212> DNA  
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 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 101  
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<210> 102  
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 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<210> 103  
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 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 103

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&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala

1

5

10

15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr

20

25

30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly

35

40

45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr

50

55

60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270

Pro Thr Thr Glu Gln Pro Val Thr Thr Phe Pro Val Thr Thr  
 275 280 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340	345	350
Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro		
355	360	365
Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu		
370	375	380
Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys		
385	390	395
Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys		
405	410	415

<210> 105  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 105  
ccgattcata gacctcgaga gt 22  
  
<210> 106  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 106  
gtcaaggagt cctccacaat ac 22  
  
<210> 107  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 107  
gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt 45  
  
<210> 108  
<211> 1838  
<212> DNA

<213> Homo sapiens

<400> 108

cggacgcgtg ggccggacgcg tggcgcccc accggcccc cgccgtggg cggtcgcttc 60  
 ttcccttcgc gtggcctacg agggtccccca gcctggtaa agatgcccc atggccccc 120  
 aagggcctag tcccgctgt gctctgggc ctcagcctct tcctcaacct cccaggac 180  
 atctggctcc agccctctcc acctccccag tcttctcccc cgcctcagcc ccatccgtgt 240  
 catacctgcc ggggactggg tgacagctt aacaaggccc tggagagaac catccggac 300  
 aactttggag gtggaaacac tgcctggag gaagagaatt tgtccaaata caaagacagt 360  
 gagaccggcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgcac 420  
 cgccctgtgg agctgagtga ggagctggg gagagctggg gtttccaaa gcagcaggag 480  
 gccccggacc tctccagtg gctgtgtca gattccctga agctctgtc ccccgccagc 540  
 accttcgggc cctccctgcct tccctgtcct gggggAACAG agaggccctg cggtgtgtac 600  
 gggcagtgta aaggagaagg gacacgaggg ggcagcgggc actgtactg ccaagccggc 660  
 tacgggggtg aggccctgtgg ccagtgtggc ctggctact ttgaggcaga acgcaacgcc 720  
 agccatctgg tatgttcggc ttgtttggc ccctgtgccc gatgctcagg acctgaggaa 780  
 tcaaactgtt tgcaatgcaaa gaaggcgtgg gccctgcac acctaagtg tgttagacatt 840  
 gatgagtgta gcacagaggg agccaaactgt ggagctgacc aattctgcgt gaacactgag 900  
 ggctcctatg agtgcgcgaga ctgtgcctag gctgcctag gctgcattggg ggcaggccca 960  
 ggtcgctgtt agaagtgttag ccctggctat cagcagggtgg gctccaagtg tctcgatgtg 1020  
 gatgagtgta agacagaggt gtgtccggga gagaacaagc agtgtaaaaa caccgaggc 1080  
 ggttatcgct gcatctgtgc cgagggtctac aagcagatgg aaggcatctg tgtgaaggag 1140  
 cagatcccag agtcagcagg cttcttcata gagatgacag aagacgagg tgggtgtctg 1200  
 cagcagatgt tcttggcat catcatctgt gcaactggcca cgctggctc taaggccgac 1260  
 ttgggtttca ccgcctatctt cattggggct gtggccggcca tgactggcta ctgggtgtca 1320  
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 gtaggacctc ctccccaccca cgctggcccc agagcttggg ctgcctctt gctggacact 1440  
 caggacagct tggtttattt ttgagagttt ggtaaagcacc cctacactgcc ttacagagca 1500  
 gcccaggatc ccaggccccgg gcagacaagg cccctgggtt aaaaagttagc cctgaagggt 1560  
 gataccatga gcttttcacc tggcgccccgac tggcaggctt cacaatgtgt gaatttcaaa 1620  
 agtttttcct taatgggtggc tgcttagagct ttggccctgt cttaggatta ggtggccctc 1680  
 acagggtgg gcccattcaca gctccctctt gccagctgca tgctggccagt tcctgttctg 1740  
 tggtttccacac atccccacac cccattgcca cttattttt catctcaggaa aataaaagaaa 1800  
 ggtttttggaa agttaaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly  
1 5 10 15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser  
                  20                     25                         30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr  
35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile  
       50                 55                 60

Arg Asp Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80  
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95  
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110  
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125  
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140  
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160  
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175  
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190  
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205  
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220  
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240  
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255  
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270  
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285  
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300  
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320  
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335  
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
 355                       360                       365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
 370                       375                       380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385                       390                       395                       400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
 405                       410                       415

Ile Lys Gly Arg  
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga           50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc   22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 112

atctgcttgt agccctcgac ac   22

<210> 113

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1461)

<223> a, t, c or g

<400> 113

tgagaccctc ctgcagccctt ctcaaggggac agccccactc tgccctttgc tcctccagg 60  
cagcaccatg cagcccctgt ggctctgtctg ggcactctgg gtgttgcccc tggccagccc 120  
cgggggccccc ctgaccgggg agcagctctt gggcagcctg ctgcggcagc tgcagctcaa 180  
agaggtgccc accctggaca gggccgacat ggaggagctg gtcatccccca cccacgttag 240  
ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300  
cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360  
gctgggttcc ggcattggagc agcggctgcc gccaacagc gagctggtgc aggccgtgct 420  
gcggctcttc caggagccgg tcccccaagggc cgcgctgcac aggcaacgggc ggtctgtcccc 480  
gcgcagcgcgc cgggccccggg tgaccgtcga gtggctgcgc gtccgcgcac acggctccaa 540  
ccgcacctcc ctcatcgact ccaggctggt gtccgtccac gagagcggct ggaaggccctt 600  
cgacgtgacc gaggccgtga acttctggca gcagctgagc cggcccccggc agccgctgtct 660  
gctacaggtg tcgggtcaga gggagcatct gggcccgctg gcgtccggcg cccacaagct 720  
ggtcccgctt gcctcgcagg gggcgccagc cgggcttggg gagcccccagc tggagctgca 780  
cacccctggac ctggggact atggagctca gggcgactgt gaccctgaag caccaatgac 840  
cgagggcacc cgctgtgtcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900  
cgagaactgg gtgctggagc ccccgccctt cctggcttat gagtgtgtgg gcacccgcgc 960  
gcagccccccg gaggccctgg ccttcaagtgc gccgttctg gggcctcgac agtgcacgc 1020  
ctcggagact gactcgctgc ccatgatcgat cagcatcaag gagggaggca ggaccaggcc 1080  
ccaggtggtc agcctgcccc acatgagggt gcagaagtgc agctgtgeet cggatggtgc 1140  
gctcgtgcca aggaggctcc agccataggc gcctagtgtt gccatcgagg gacttgactt 1200  
gtgtgtgttt ctgaagtgtt cgagggtaacc aggagagctg gcgatgactg aactgctgat 1260  
ggacaaaatgc tctgtgtctt ctgtgagcc ctgaatttgc ttccctgtac aagttaccc 1320  
acctaatttt tgcttctcag gaatgagaat cttggccac tggagagccc ttgctcagg 1380  
ttctctattt ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440  
acctgagggc agaaaagccca ntgtgtcatt gtttacttgt cctgtcaactg gatctgggt 1500  
aaagtccctcc accaccactc tggacctaag acctgggggt aagtgtgggt tgcaccc 1560  
caatccaaqat aataaaagact ttgtaaaaaca tgaataaaaac acattttattt ctaaaa 1616

<210> 114

<211> 366

<212> PRT

<213> Homo sapiens

<400> 114

Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
1 5 10 15

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
20 25 30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
       50                     55                     60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
       65                     70                     75                     80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
       85                     90                     95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
       100                    105                    110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
       115                    120                    125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
       130                    135                    140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
       145                    150                    155                    160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
       165                    170                    175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
       180                    185                    190

Pro Arg Gln Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
       195                    200                    205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
       210                    215                    220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
       225                    230                    235                    240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
       245                    250                    255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
       260                    265                    270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
       275                    280                    285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
       290                    295                    300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
       305                    310                    315                    320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
       325                    330                    335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 115

aggactgccat taacttgccct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 116

ataggagttt aaggcaggcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgcattaccgc tactgccaggc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtccctt cggccggctgt ttttgtcagtg gcctgatcgatc gatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcataat tggcgatcct gtttgtgctcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcaaat ttctgagaat 180

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaaag 240  
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300  
gaggaccggg tgacccctt gccaactgtt atcaccttca agtccgtgac acgggaagac 360  
actgggacat acacttgtat ggtctcttag gaaggcggca acagctatgg ggagggtcaag 420  
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctccctgtcc 480  
accattggg accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540  
tacaccttgtt tcaaagatgg gatagtgtat cctacgaatc caaaaagcac cctgtgccttc 600  
agcaactctt cctatgtcct gaatcccaca acaggagagc tggctttga tccccgtgtca 660  
gcctctgata ctggagaata cagctgttag gcacggaatg ggtatggac acccatgact 720  
tcaaattgtcg tgcgcattggg agctgtggag cggaatgtgg gggtcatcggt ggcagccgtc 780  
cttgcataccc tgattctcct gggaatcttg gttttggca tctgggttgc ctatagccga 840  
ggccactttg acagaacaaa gaaaggact tcgagtaaga aggtgattta cagccagcct 900  
agtgcggaa gtgaaggaga attcaaacag acctcgcat tcctgggtgt agcctggtcg 960  
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tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cttccctccc 1140  
tttccttacca ctgctgagtg gcctggaaact tgtttaaagt gtttattccc catttctttg 1200  
agggatcagg aaggaatcct gggtatgcca ttgacttccc ttctaagtag acagaaaaaa 1260  
tggcgggggt cgccaggatc tgcactcaac tgccccatcg gctggcaggg atctttgaat 1320  
aggtatctt agcttggttc tgggctctt cttgtgtac tgacgaccag gcccagctgt 1380  
tctagagccg gaatttagagg cttagagccg tgaaatgggt gtttgggtat gacactgggg 1440  
tccttcacat tctggggccc actctcttct gtcttcccat gggaaatgtgcc actgggatcc 1500  
ctctgccttg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt gaaaaatggg 1560  
agctctgtt gtggagagca tagtaaattt tcaagagaact tgaagccaaa aggatttaaa 1620  
accgctgctc taaagaaaaag aaaactggag gctgggcgcgat gttggctacg cctgtatcc 1680  
cagaggctga ggccaggccgat tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740  
ggagaaaaccc tactggaaat acaaagtttgc ccaggcatgg tgggtgcgtc ctgtgttccc 1800  
agctgctcag gggccctggca acaagagcaa aactccagct caaaaaaaaaaa aaaaaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Gly Ile Leu Val Phe Gly  
 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 121		
tgatcgcgat ggggacaaag gcgcaggctc gagaggaaac tgttgtgcct		50
<210> 122		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 122		
acacctgggtt caaagatggg		20
<210> 123		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 123		
taggaagagt tgctgaaggc acgg		24
<210> 124		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 124		
ttgccttact caggtgctac		20
<210> 125		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		

## oligonucleotide probe

<400> 125  
 actcagcagt ggttagaaag 20

<210> 126  
 <211> 1210  
 <212> DNA  
 <213> Homo sapiens

<400> 126  
 cagcgcgtgg ccggcgccgc tgggggaca gcatgagcgg cggttggatg gcgcagggtt 60  
 gagcgtggcg aacaggggct ctggccctgg cgctgctgt gctgctcgcc ctcggactag 120  
 gcctggaggc cggcgcgagc cccgtttcca ccccgcacca tgcccaggcc gcaggcccc 180  
 gtcaggctc gtgcccaccc accaagtcc agtgcgcac cagtgctta tgcgtgcccc 240  
 tcacctggcg ctgcgacagg gacttggact gcaagcgatgg cagcgatgag gaggagtgc 300  
 ggattgagcc atgtaccacaa aaagggcaat gcccaccgccc ccctggcctc ccctgccc 360  
 gcacccggcgt cagtactgc tctggggaa ctgacaagaa actgcgcacac tgcagccccc 420  
 tggcctgcct agcaggcgag ctccgttgc cgcgtggca tgactgcatt ccactcacgt 480  
 ggcgtgcga cggccaccca gactgtcccg actccagcga cgagctcgcc tggaaacca 540  
 atgagatcct cccggaaggg gatgccacaa ccatgggccc ccctgtgacc ctggagagt 600  
 tcacctctc caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtccct 660  
 ctgtcggaa tgccacatcc tcctctgccc gagaccatgc tggaaacccca actgcctatg 720  
 gggttattgc agctgctgcg gtgctcagtg caagcctgtt caccgcacc tcctctt 780  
 tgcgtggct ccgagccca gaggccctcc gcccacttgg gttactggtg gccatgaagg 840  
 agtcctgct gctgtcagaa cagaagaccc cgcgtccctg aggacaagca cttgccacca 900  
 ccgtcactca gcccctggcg tagccggaca ggaggagagc agtgcgcgg atgggtaccc 960  
 gggcacacca gcccctcagag acctgagttc ttctggccac gtgaaacccca gaacccggc 1020  
 tcctgcagaa gtggccctgg agattgaggg tccctggaca tccttatgg agatccgggg 1080  
 agcttagatg gggAACCTGC cacagccaga actgaggggc tggcccccagg cagctccca 1140  
 ggggtagaac gcccctgtgc ttaagacact ccctgtgcc cctgtgagg gtggcgattt 1200  
 aagttgttcc 1210

<210> 127  
 <211> 282  
 <212> PRT  
 <213> Homo sapiens

<400> 127  
 Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
       1                  5                  10                  15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
       20                  25                  30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
       35                  40                  45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
       50                  55                  60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
       65                  70                  75                  80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                   85                      90                      95  
  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                   100                    105                      110  
  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                   115                    120                      125  
  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                   130                    135                      140  
  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                   145                    150                      155                  160  
  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                   165                    170                      175  
  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                   180                    185                      190  
  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                   195                    200                      205  
  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                   210                    215                      220  
  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala  
                   225                    230                      235                  240  
  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                   245                    250                      255  
  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                   260                    265                      270  
  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                   275                    280  
  
 <210> 128  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe  
  
 <400> 128  
 aagttccagt gccgcaccag tggc  
  
 <210> 129



cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggcaggatg ttccagacca 1200  
 agttcaaggc ccacttccc cccaggggc ctccccggag ttccagcagt gaccctgact 1260  
 ttgtggtgtt agacggcggt cccgtcatgc tcccgtctta tgacgaagct gtgagtggcg 1320  
 gcttgagtgc cttaggcccc gggtacatgg cctctgtggg ccagggctgc cccttacccg 1380  
 tggacgacca gagcccccca gcataccccc gtcagggga cacggacaca ggcccagggg 1440  
 agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500  
 ctcccagggtg ccaagagagc acccaccctg cttcggacaa ccctgacata attgccagca 1560  
 cggcagagga ggtggcatcc accagcccag gcatccatca tgcccactgg gtgttgtcc 1620  
 taagaaaactg attgattaaa aaatttccca aagtgtctg aagtgtctct tcaaatacat 1680  
 gttgatctgt ggagtgttatt ccttccttc tcttggttt agacaaatgt aaacaaagct 1740  
 ctgatccta aaattgctat gctgatagag tggtgagggc tggaagctt atcaagtcct 1800  
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
1				5				10					15		

Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
					20			25				30		

Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
					35			40				45			

Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
					50			55			60				

Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
					65				70		75			80	

Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
					85				90			95			

Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
					100				105			110			

Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
					115				120			125			

Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
					130			135			140				

Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
							145		150			155		160	

Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
					165				170			175			

Cys	Gln	Gly	Cys	Leu	Arg	Pro	Leu	Ala	Ser	Ser	Asn	Gly	Tyr	Val	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
245	250	255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
260	265	270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465                          470                          475                          480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485                          490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133

atctcctatc gctgcttcc cggt

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135

atttaaaactt gatgggtctg cgtatcttga gtgcttacaa aaccatatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

ccccacgcgtc cgctccgcgc cctccccccc gcctcccgtg cggccgtcg gtggcctaga 60  
 gatgctgctg ccgcgggtgc agttgtcgcg cacgcctctg cccgccagcc cgctccacccg 120  
 ccgttagcgcc cgagtgtcgg gggcgccacc cgagtcgggc catgaggccg ggaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgcctgc 240  
 tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccggga gggacacaga 300

ggccttgta taaagtccatt tacttccatg atacttctcg aagactgaac ttggagaaag 360  
ccaaaagaagc ctgcaggagg gatggaggcc agctagtca catcgagtct gaagatgaac 420  
agaaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtac ttctggattg 480  
ggctcaggag gcgtgaggag aaacaagaac atagcacagc ctgccaggac ctttatgctt 540  
ggactgatgg cagcatatca caattttagga actggatgt ggatgagccg tcctgcccga 600  
gcgaggctg cgtggatcatg taccatcagc catcgccacc cgctggcattc ggaggcccct 660  
acatgttcca gtggaatgtat gaccggtgca acatgaagaa caatttcatt tgcaaataatt 720  
ctgatgagaa accagcagtt ccttcttagag aagctgaagg tgagggaaaca gagctgacaa 780  
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaaagta 840  
gagaagctgc cttgaatctg gcctacatcc taatccccag cattccctt ctccctccctt 900  
ttgtggtcac cacagttgtat tggtgggtt ggatctgttag aaaaagaaaa cgggagcagc 960  
cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag gaaaacagcc 1020  
cgacccatga ggcttacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080  
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tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggtt gtgactctgg 1200  
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tccagctcga ccttatgaga aggtacccctg cccaggtctg gcacatagta gagtctcaat 1560  
aaatgtcact tgggtggatg tatctaactt ttaagggaca gagcttacc tggcagtgtat 1620  
aaagatgggc tggagactt ggaaaaccac ctctgttttc cttgccttat acagcagcac 1680  
atattatcat acagacagaa aatccagaat cttttcaaaag cccacatatg gtagcacaagg 1740  
ttggcctgtg catcgccaaat tctcatatct gttttttca aagaataaaa tcaaataaa 1800  
aqaqaaaaaaa aaaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val 10 Leu Leu Ala Val 15 Leu

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
           100                  105                  110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 138  
 gttcattgaa aacctttgc catgtatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 140  
 cagtccaagc ataaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcattccgcag gttcccgggg acttgggggc gccccgttag ccccgccgcg cgcagaagac 120  
 ttgtgtttgc ctccctgcaggc ctcaacccgg agggcagcga gggcttacca ccatgtatcac 180  
 tggtgtgttc agcatgcgtct tgtggacccc agtggggcgctc ctgacccctgc tggcgtactg 240  
 cctgcaccag cggcggttgg cccttgccga gctgcaggag gccatggcc agtgtccgg 300  
 cgaccgcagc ctgctgaagt tgaaaatggc gcaggtcggt tttcgacacg gggctcgag 360  
 tcctctcaag ccgcctccgc tggaggagca ggttagagtgg aaccccccagc tattagaggt 420  
 cccaccccaa actcagtttgc attacacagt caccaatcta gctgggtggc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctggca 540  
 gctgaccaag gtgggcattgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600  
 tgtggaaagac attcccttgc tttcaccaac cttcaaccca caggaggtct ttattcggttc 660  
 cactaacatt tttcgaaatc tggagtccac ccgttgggttgc ctggctggc tttccagtg 720

tcagaaaagaa ggaccatca tcatccacac tgatgaagca gattcagaag tcttgatcc 780  
 caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840  
 tttacagcca ggaatctcg aggatttcaa aaaggtgaag gacaggatgg gcattgacag 900  
 tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960  
 cctcccaagc tgccccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020  
 cacatccttgc tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtaggccc 1080  
 attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140  
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200  
 gaccctgggg attttgacc acaaatggcc accgtttgtt gttgaccta ccattgaaact 1260  
 ttaccagcac ctggaatcta aggagtgggt tttgcagtc tattaccacg ggaaggagca 1320  
 ggtgccgaga gttgcctg atggctctg cccgctgac atgttcttga atgcattgtc 1380  
 agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440  
 agttggaaat gaagagtaac tgatttataa aagcaggatg ttttgatttt aaaataaaagt 1500  
 gccttataac aatg 1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met	Ile	Thr	Gly	Val	Phe	Ser	Met	Arg	Leu	Trp	Thr	Pro	Val	Gly	Val
1				5					10				15		

Leu	Thr	Ser	Leu	Ala	Tyr	Cys	Leu	His	Gln	Arg	Arg	Val	Ala	Leu	Ala
								20				25		30	

Glu	Leu	Gln	Glu	Ala	Asp	Gly	Gln	Cys	Pro	Val	Asp	Arg	Ser	Leu	Leu
								35				40		45	

Lys	Leu	Lys	Met	Val	Gln	Val	Val	Phe	Arg	His	Gly	Ala	Arg	Ser	Pro
			50				55				60				

Leu	Lys	Pro	Leu	Pro	Leu	Glu	Gln	Val	Glu	Trp	Asn	Pro	Gln	Leu
	65				70				75			80		

Leu	Glu	Val	Pro	Pro	Gln	Thr	Gln	Phe	Asp	Tyr	Thr	Val	Thr	Asn	Leu
					85				90			95			

Ala	Gly	Gly	Pro	Lys	Pro	Tyr	Ser	Pro	Tyr	Asp	Ser	Gln	Tyr	His	Glu
				100				105				110			

Thr	Thr	Leu	Lys	Gly	Gly	Met	Phe	Ala	Gly	Gln	Leu	Thr	Lys	Val	Gly
						115				120			125		

Met	Gln	Gln	Met	Phe	Ala	Leu	Gly	Glu	Arg	Leu	Arg	Lys	Asn	Tyr	Val
			130				135				140				

Glu	Asp	Ile	Pro	Phe	Leu	Ser	Pro	Thr	Phe	Asn	Pro	Gln	Glu	Val	Phe
	145				150				155			160			

Ile	Arg	Ser	Thr	Asn	Ile	Phe	Arg	Asn	Leu	Glu	Ser	Thr	Arg	Cys	Leu
					165				170			175			

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
                  180   185                                 190  
  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
                  195   200                                 205  
  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
                  210   215                                 220  
  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
                  225   230                                 235                                 240  
  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
                  245   250                                 255  
  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
                  260   265                                 270  
  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
                  275   280                                 285  
  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
                  290   295                                 300  
  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
                  305   310                                 315                                 320  
  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
                  325   330                                 335  
  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
                  340   345                                 350  
  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
                  355   360                                 365  
  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
                  370   375                                 380  
  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
                  385   390                                 395                                 400  
  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
                  405   410                                 415  
  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
                  420   425

<210> 143  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 143
      ccaactacca aagctgctgg agcc                                24

<210> 144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 144
      gcagctctat taccacggga agga                                24

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 145
      tccttcccggt ggtaatagag ctgc                                24

<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 146
      ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg      45

<210> 147
<211> 1686
<212> DNA
<213> Homo sapiens

<400> 147
      ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttcttagc 60
      cttaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat tctcattgtat 120
      cttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180

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gggcctccac cgctgtgaag ggcgggtgga ggtgaaacag aaaggccagt ggggcacctg 240  
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgtt tgccgggagc tgggctgtgg 300  
agctgccagc ggaaccccta gtggtattt gtatgagcca ccagcagaaa aagagcaaaa 360  
ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420  
agaagaagtt tatgattgtt cacatgatga agatgctggg gcattgtgt agaacccaga 480  
gagctttc tccccagtcc cagagggtgt caggctggct gacggccctg ggcattgcaa 540  
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600  
cctccgggccc gcaaagggtgg tgtgcggca gctgggatgt gggagggctg tactgactca 660  
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caaccatgtt gaagacacgt gggtgaatgg tgaagatccc ttgacttga gacttagg 840  
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ctggctggat aatgttctgtt gctcaggggaa ggagcagtcc ctggagcagt gccagcacag 1080  
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<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

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                   20                  25                  30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
           50                     55                     60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65                   70                   75                   80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
     115                       120                       125  
  
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
     130                       135                       140  
  
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
     145                       150                       155                   160  
  
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
     165                       170                       175  
  
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
     180                       185                       190  
  
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
     195                       200                       205  
  
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
     210                       215                       220  
  
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
     225                       230                       235                   240  
  
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
     245                       250                       255  
  
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
     260                       265                       270  
  
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
     275                       280                       285  
  
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
     290                       295                       300  
  
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
     305                       310                       315                   320  
  
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
     325                       330                       335  
  
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
     340                       345  
  
 <210> 149  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 149		
ttcagctcat cacccatccc tgcc		24
<210> 150		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 150		
ggctcataca aaataccact aggg		24
<210> 151		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 151		
gggcacctccac cgctgtgaag ggcgggtgga ggtggAACAGGAAAGCCAGT		50
<210> 152		
<211> 1427		
<212> DNA		
<213> Homo sapiens		
<400> 152		
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gaaggtgtaaag gccatggact tcatcacccac cacagccatc ctgcggccctgc tggtcggtcg 180		
cctggggcgtc ttccggccctt tccggctgtgc gcagtgggtg cgccggaaagg cctaccccg 240		
gaatgctgtg gtgggtatca caggccac ctcaggccgt ggcaaaagaat gtgcggaaatgt 300		
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ggtgacccctc gacccacacg actctggggc catagttgca gcagcagctg agatcctgca 480		
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<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

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Leu	Gly	Val	Phe	Gly	Leu	Phe	Arg	Leu	Leu	Gln	Trp	Val	Arg	Gly	Lys
															30
20															

Ala	Tyr	Leu	Arg	Asn	Ala	Val	Val	Val	Ile	Thr	Gly	Ala	Thr	Ser	Gly
35															45

Leu	Gly	Lys	Glu	Cys	Ala	Lys	Val	Phe	Tyr	Ala	Ala	Gly	Ala	Lys	Leu
50															60

Val	Leu	Cys	Gly	Arg	Asn	Gly	Gly	Ala	Leu	Glu	Glu	Leu	Ile	Arg	Glu
65															80

Leu	Thr	Ala	Ser	His	Ala	Thr	Lys	Val	Gln	Thr	His	Lys	Pro	Tyr	Leu
85															95

Val	Thr	Phe	Asp	Leu	Thr	Asp	Ser	Gly	Ala	Ile	Val	Ala	Ala	Ala	
100															110

Glu	Ile	Leu	Gln	Cys	Phe	Gly	Tyr	Val	Asp	Ile	Leu	Val	Asn	Asn	Ala
115															125

Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Ile	Met	Asp	Thr	Thr	Val	Asp	Val	Asp
130															140

Lys	Arg	Val	Met	Glu	Thr	Asn	Tyr	Phe	Gly	Pro	Val	Ala	Leu	Thr	Lys
145															160

Ala	Leu	Leu	Pro	Ser	Met	Ile	Lys	Arg	Arg	Gln	Gly	His	Ile	Val	Ala
165															175

Ile	Ser	Ser	Ile	Gln	Gly	Lys	Met	Ser	Ile	Pro	Phe	Arg	Ser	Ala	Tyr
180															190

Ala	Ala	Ser	Lys	His	Ala	Thr	Gln	Ala	Phe	Phe	Asp	Cys	Leu	Arg	Ala
195															205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235
Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
245	250	255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val		
260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
290	295	300
Arg Lys Ser Lys Asn Ser		
305	310	

<210> 154  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 154  
ggtgctaaac tggtgctctg tgga 24

<210> 155  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 155  
cagggcaaga tgagcattcc 20

<210> 156  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 156		
tcatactgtt ccatctcgcc acgc		24
<210> 157		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
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<210> 158		
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<212> DNA		
<213> Homo sapiens		
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<210> 159		

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Ile	Val
1															15

Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
															30
		20					25								

Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
															45
								40							

Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
															60
		50				55									

Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
															80
		65				70			75						

Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
															95
							85			90					

Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
															110
		100					105								

Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
															125
		115					120								

Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
															140
		130				135									

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
															160
		145			150			155							

Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
															175
			165				170								

Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
															190
				180			185								

Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
															205
		195				200									

Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
															220
		210			215										

Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
															240
		225			230			235							

Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
															255
			245			250			250						



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 gaaataaaaaa tattatatat aaaagtaaaaa aaaaaaaaaa 2076

&lt;210&gt; 164

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met

1

5

10

15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser

20

25

30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr

35

40

45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly

50

55

60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln			
85	90	95	
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100	105	110	
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115	120	125	
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130	135	140	
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145	150	155	160
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165	170	175	
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180	185	190	
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195	200	205	
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210	215	220	
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225	230	235	240
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245	250	255	
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260	265	270	
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275	280	285	
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290	295	300	
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305	310	315	320
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325	330	335	
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340	345	350	

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
 370                    375                    380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
                   405                  410                  415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> De:

oligonucleotide probe

<400> 165

tccatggca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 166

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24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 167
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<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 168
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<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens

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&lt;210&gt; 170

&lt;211&gt; 552

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 170

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							20				25		30		

Gln	Pro	Gly	Lys	Val	Glu	Gln	Met	Ser	Thr	His	Arg	Ser	Arg	Leu	Leu
							35				40		45		

Thr	Ala	Ala	Pro	Leu	Ser	Met	Glu	Gln	Arg	Gln	Pro	Trp	Pro	Arg	Ala
						50				55		60			

Leu	Glu	Val	Asp	Ser	Arg	Ser	Val	Val	Leu	Leu	Ser	Val	Val	Trp	Val
							65			70		75		80	

Leu	Leu	Ala	Pro	Pro	Ala	Ala	Gly	Met	Pro	Gln	Phe	Ser	Thr	Phe	His
							85			90		95			

Ser	Glu	Asn	Arg	Asp	Trp	Thr	Phe	Asn	His	Leu	Thr	Val	His	Gln	Gly
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Thr	Gly	Ala	Val	Tyr	Val	Gly	Ala	Ile	Asn	Arg	Val	Tyr	Lys	Leu	Thr
							115			120		125			

Gly	Asn	Leu	Thr	Ile	Gln	Val	Ala	His	Lys	Thr	Gly	Pro	Glu	Glu	Asp
							130			135		140			

Asn	Lys	Ser	Arg	Tyr	Pro	Pro	Leu	Ile	Val	Gln	Pro	Cys	Ser	Glu	Val
							145			150		155		160	

Leu	Thr	Leu	Thr	Asn	Asn	Val	Asn	Lys	Leu	Leu	Ile	Ile	Asp	Tyr	Ser
							165			170		175			

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 180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
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Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
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Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

100

450                          455                          460  
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465                          470                          475                          480  
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
485                          490                          495  
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
500                          505                          510  
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
515                          520                          525  
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
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Leu Tyr Phe Leu Gly Glu Gln Arg  
545                          550

<210> 171  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171  
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<210> 172  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172  
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<210> 173  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD RES

222 <222> (539)

<223> Any amino acid

<400> 175

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20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln  
35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe  
50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp  
                 65                      70                      75                      80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr  
85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser  
100 105 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly  
           115                  120                  125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp  
130 135 140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160  
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175  
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
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 305 310 315 320  
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 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
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 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
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 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
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 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
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Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
 450                          455                          460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
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Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
 485                          490                          495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
 500                          505                          510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
 515                          520                          525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
 530                          535                          540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
 545                          550                          555                          560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
 565                          570                          575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
 580                          585                          590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
 595                          600                          605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
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Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
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<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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ggtggtcat gcctgtatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280  
tcaggacttc aagaccagcc tggccaaacat ggtgaaaccc cgtctccact aaaaatacaa 2340  
aaattagccg ggcgtgtatgg tggcacccctc taatcccacg tacttggag gctgaggggca 2400  
ggagaattgc ttgaatccag gaggcagagg ttgcagttag tggaggttgc accactgcac 2460  
tccagccctgg ctgacagtga gacactccat ctcaaaaaaaa aaaaa 2505

&lt;210&gt; 177

&lt;211&gt; 654

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu

1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val

20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr

35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala

50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175

Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190

Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205

Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220

Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Val Asp Phe Gly Pro  
 225 230 235 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
405	410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
420	425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
485	490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178  
tggctactcc aagaccctgg catg 24

<210> 179  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179  
tggacaaaatc cccttgctca gccc 24

<210> 180  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180  
gggcttcacc gaaggcagtgg acctttatgg tgaccacctg atgtccaggg 50

<210> 181  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181  
ccagctatga ctatgatgca cc 22

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<210> 182
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 182
tggcacccag aatggtgttg gctc                                         24

<210> 183
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 183
cgagatgtca tcagcaagtt ccaggaagtt ctttggac cttaacctcc                                         50

<210> 184
<211> 1947
<212> DNA
<213> Homo sapiens

<400> 184
gctttgaaca cgtctgcaag cccaaagtt agcatctgat tggtatgag gtatttgagt 60
gcaccaccaa tatggcttac atgttaaaaa agcttctcat cagttacata tccattattt 120
gtgttatgg ctttatctgc ctctacactc tcttcgttt attcaggata ccttgaagg 180
aatattctt cggaaaaagtc agagaagaga gcagtttag tgacattcca gatgtcaaaa 240
acgattttgc gttccttctt cacatggtag accagttatga ccagctatat tccaagcggt 300
ttggtgtgtt cttgtcagaa gtttagtggaaa ataaacttag ggaaatttagt ttgaaccatg 360
agtggacatt tgaaaaaactc aggacgcaca tttcacgcaa cgcccaggac aagcaggagt 420
tgcattgtt catgctgtcg ggggtgcccg atgctgttt tgacattcaca gacctggatg 480
tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagattct caaatgacta 540
acctccaaga gctccacctc tgccactgcc ctgcaaaaat tgaacagact gcttttagct 600
ttcttcgca tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattccctg 660
cctgggtgtt ttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
aaaacaataa gatgatagga cttgaatctc tccgagagtt gcccacctt aagattctcc 780
acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840
caaagtttagt cattcataat gacggcacta aactcttggt actgaacagc cttaaagaaaa 900
tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960
tttcagcct ctctaaattt caggaactgg atttaaagtca caataacatt cgcacaattt 1020
aggaaatcat cagtttccag cattttaaac gactgacttg tttaaaaatta tggcataaca 1080
aaattgttac tatttcctccc tcttattaccc atgtcaaaaaa cttggagtca ctttatttct 1140
ctaaacaaca gctcgaatcc ttaccagtgg cagtttttag tttacagaaaa ctcagatgct 1200
tagatgtgag ctacaacaac atttcaatga ttccaaataga aataggattt cttcagaacc 1260
tgcagcattt gcatatcact gggaaacaag tggacattct gccaaaacaa ttgtttaaat 1320

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gcataaaagtt gaggactttg aatctgggac agaactgcat cacctcaactc ccagagaaaag 1380  
 ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440  
 cagcccagct gggccagtgt cgatgctca agaaaagcgg gcttgggttg gaagatcacc 1500  
 ttttgatac cctgccactc gaagtcaaag aggcatgaa tcaagacata aatattccct 1560  
 ttgcaaatgg gatttaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620  
 agattgcaag tgctcacgta caagttatta caagataatg cattttagga gtagatacat 1680  
 cttttaaaat aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740  
 aatgttgta gggtttaag tcattcattt ccaaattcatt ttttttttc ttttggggaa 1800  
 agggaaaggaa aaattataat cactaatctt gttctttt aaattgtttg taacttggat 1860  
 gctgccgcta ctgaatgtt acaaattgct tgcctgctaa agtaaatgat taaattgaca 1920  
 ttttcttact aaaaaaaaaaaaaaaa 1947

&lt;210&gt; 185

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

Met	Ala	Tyr	Met	Leu	Lys	Lys	Leu	Leu	Ile	Ser	Tyr	Ile	Ser	Ile	Ile
1									10					15	

Cys	Val	Tyr	Gly	Phe	Ile	Cys	Leu	Tyr	Thr	Leu	Phe	Trp	Leu	Phe	Arg
									25					30	

Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser
									40					45	

Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His
									55					60	

Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
									75					80	

Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His
									90					95	

Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln
								105					110		

Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala
								115					120		125

Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro
								130					135		140

Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu
								145					150		160

Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser
								165					170		175

Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val
								180					185		190

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465                          470                          475                          480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro  
485                          490                          495

Phe Ala Asn Gly Ile  
500

<210> 186

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 186

cctccctcta ttacccatgt c

21

<210> 187

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 187

gaccaacttt ctctggagt gagg

24

<210> 188

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 188

gtcactttat ttctctaaca acaagctcga atccttacca gtggcag

47

<210> 189

<211> 2917

<212> DNA

<213> Homo sapiens

<400> 189

ccccacgcgtc cggccttctc tctggacttt gcatttccat tcctttcat tgacaaactg 60  
actttttta tttttttt tccatctcg ggccagcttgg gatcctagg cgccctggg 120  
aagacatttg tggtttacac acataaggat ctgtgtttgg gtttcttct tcctccctg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240  
 gcacttatct gccttaggtac atcgaagtct tttgacctcc atacagtat tatgcctgtc 300  
 atcgctggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtcttac 360  
 ttcaaaaatac aacaacgcgt aaaagctgca aaggaacctg aagctgtggc tgaaaaaaat 420  
 cacaacccag acaagggtgtg gtgggccaag aacagccagg ccaaaaccat tgccacggag 480  
 tcttgcctg ccctgcagtg ctgtgaagga tatagaatgt gtgcagttt tgattccctg 540  
 ccacccgt gttgcacat aaatgagggc ctctgaggtt gggaaaggctc ccttctcaaa 600  
 gcagagccct gaagacttca atgatgtcaa tgaggccacc tggttgtat gtgcaggcac 660  
 agaagaaaagg cacagctccc catcagttc atggaaaata actcagtgcc tgctggAAC 720  
 cagctgctgg agatccctac agagagctc cactggggc aacccttcca ggaaggagtt 780  
 ggggagagag aaccctcaact gtggggaaatg ctgataaaacc agtcacacag ctgctctatt 840  
 ctcacacaaa tctaccctt gcgtggctgg aactgacggtt tccctggagg tgcacccaaa 900  
 gctgatgtaa cacagagccct ataaaagctg tcggcctta aggctgccc ggccttgcc 960  
 aaaatggagc ttgtaaaaag gctcatgcca ttgaccctct taattctctc ctgtttggcg 1020  
 gagctgacaa tggcgaggc tgaaggcaat gcaagctgca cagtcagttt aggggggtgccc 1080  
 aatatggcag agacccacaa agccatgatc ctgcaactca atcccaactgaa gaactgcacc 1140  
 tggacaatag aaagaccaga aaacaaaagc atcagaattt tctttccctt tgccagctt 1200  
 gatccagatg gaagctgtgaa aagtggaaac attaaagtct ttgacggaaac ctccagcaat 1260  
 gggccctctgc tagggcaagt ctgcagttt aacgactatg ttccctgtatt tgaatcatca 1320  
 tccagtagat tgcgtttca aatagttact gactcagccaa gaattcaaaag aactgtctt 1380  
 gtcttctact acttcttctc tcctaaccatc tctattccaa actgtggcg ttacctggat 1440  
 accttggaaag gatccttcac cagccccaaat tacccttcaaa cgcattctgaa gctggcttat 1500  
 tgtgtgtggc acatacaagt ggagaaaagat tacaagataa aactaaactt caaagagatt 1560  
 ttcttagaaaa tagacaaaaca gtgcaaaattt gattttcttg ccatttatgaa tggccccctcc 1620  
 accaactctg gcctgattgg acaagtctgtt gcccgtgtaa ctcccacctt cgaatcgatca 1680  
 tcaaactctc tgactgtcgat gttgtctaca gattatgoca attcttaccg gggattttct 1740  
 gcttcctaca cctcaattt tgcagaaaac atcaacacta catctttaac ttgctctct 1800  
 gacaggatga gagttattat aagcaaatcc taccttaggg cttttaactc taatggaaat 1860  
 aacttgcac taaaagaccc aacttgcaga cccaaattat caaatgttgc ggaattttct 1920  
 gtccttcata atggatgtgg tacaatcaga aaggttagaaat atcagtcaat tacttacacc 1980  
 aatataatca cctttctgc atcctcaact tctgaagtgtca tcaccctgtca gaaacaactc 2040  
 cagattattt tgaagtgtgaa atggggacat aattctacag tggagataat atacataaca 2100  
 gaagatgtg taatacaaaag tcaaaaatgca ctggggcaaat ataacaccag catggcttt 2160  
 ttgaatcca attcatttga aaagactata tctgaatcacatcatattatgt ggatttgaac 2220  
 caaactctt ttgttcaagt tagtctgcac acctcagatc caaatttggg ggtgtttctt 2280  
 gataacctgta gaggcctctcc cacctctgac tttgcatctc caacccatcgaa cctaattcaag 2340  
 agtggatgtt gtcgagatgtt aacttgcataag gtgtatccct tatttggaca ctatgggaga 2400  
 ttccagtttta atgcctttaa attcttgcata aagttgatgtt ctgtgtatct gcagtgtaaa 2460  
 gttttgatgtt gtgatagcag tgaccaccag tctcgctgca atcaagggtt tgctccaga 2520  
 agcaaaacggg acattttctt atataaaatgg aaaacagatt ccattatagg acccattcgt 2580  
 ctgaaaagggtt atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgcgaa 2640  
 gaaaactccaa accagccctt caacagtgtt catctgtttt ccttcatgtt tctagctctg 2700  
 aatgtgggtt ctgttagcgac aatcacagtg aggcatggg taaatcaacg ggcagactac 2760  
 aaataccaga agctgcagaaa ctattaacta acaggtccaa ccctcaactgaa gacatgtttc 2820  
 tccaggatgc caaaggaaat gctaccctgtt ggctacacat attatgaata aatgagggaaag 2880  
 ggcctgaaaag tgacacacacat gcctgcattt aaaaaaaaaa 2917

&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110

Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140

Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160

Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175

Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190

Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205

Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220

Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240

Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255

Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270

Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300  
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350  
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365  
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430  
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445  
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

	565	570	575
Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe			
580	585		590
Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr			
595	600		605
<210> 191			
<211> 21			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic			
oligonucleotide probe			
<400> 191			
tctctattcc aaactgtggc g			21
<210> 192			
<211> 22			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic			
oligonucleotide probe			
<400> 192			
tttgatgacg attcgaaggt gg			22
<210> 193			
<211> 47			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic			
oligonucleotide probe			
<400> 193			
ggaaggatcc ttcaccagcc ccaattaccc aaagccgcac cctgagc			47
<210> 194			
<211> 2362			
<212> DNA			
<213> Homo sapiens			
<400> 194			
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cgggacatgc ggccccagga gctccccagg ctcgcgttcc cgttgctgtct gttgctgttg 120			
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gagtcctcgg acgcccgcga gctgcccccg 240  
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<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

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Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr  
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Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala  
                  35                 40                 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
 50 55 60  
 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
 65 70 75 80  
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95  
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
 100 105 110  
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125  
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
 130 135 140  
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160  
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175  
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190  
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205  
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220  
 Leu Trp Ser Asp Gly Asp Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240  
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255  
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270  
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285  
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300  
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320  
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
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Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
 450 455 460

Asn Val Ile  
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cggtt

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 197

ggattccatcc tcaaggaaga gcgg

24

<210> 198

<211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe  
  
 <400> 198  
 aacttgcagc atcagccact ctgc 24

<210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe  
  
 <400> 199  
 ttccgtgccc agcttcggta gcgagtggtt ctggtggtat tggca 45

<210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens  
  
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 catctgaggt gttccctgg ctctgaaggg gtggcacga tggccagggt cttcagctg 180  
 gtgttgccttc tcacttccat ctggaccacg aggctcctgg tccaaggctc tttgcgtgca 240  
 gaagagcttt ccatccaggt gtcatgcaga attatgggta tcacccttgt gagaaaaaag 300  
 gcgaaaccagc agctgaatt cacagaagct aaggaggcct gttaggtgtc gggactaagt 360  
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caaatgtatc actagccctc cttttccaa caagaaggga ctgagagatg cagaaatatt 2340  
tqtqacaaaa aattaaagca ttttagaaaaac tt 2372

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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20 25 30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala  
35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu  
50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala  
65                   70                   75                   80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val  
85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys  
115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile  
 130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 202  
 gagcttcca tccaggtgtc atgc 24

<210> 203  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 203		
gtcagtgaca gtacctactc gg		22
<210> 204		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 204		
tggagcagga ggagtagtag tagg		24
<210> 205		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
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aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt		50
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<212> DNA		
<213> Homo sapiens		
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<223> a, t, c or g		
<220>		
<221> modified_base		
<222> (977)		
<223> a, t, c or g		
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<221> modified_base		
<222> (996)		
<223> a, t, c or g		
<220>		
<221> modified_base		

&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

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&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

1 5 10 15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu

20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65 70 75 80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
 85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
 100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
 115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
 130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
 145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
 165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
 180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
 195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
 210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
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Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
 245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
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Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
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Asp Gly Glu Asn Lys Lys Asp Lys  
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<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 208

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<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 211  
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<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
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<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

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Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
 35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
           100             105             110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr 130	135	140
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu 145	150	155
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg 165	170	175
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala 180	185	190
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly 195	200	205
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr 210	215	220
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro 225	230	235
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp 245	250	255
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu 260	265	270
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu 275	280	285
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys 290	295	300
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser 305	310	315
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu 325	330	335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr 340	345	350
Gly Val Tyr Cys Tyr Arg Gln His 355	360	
<210> 214		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 215

ttcccttgtg ggttggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 216

agggcgtggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 217

agccagttag gaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 218

tgtccaaagt acacacacctt gagg

24

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<210> 219
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 219
gatgccacga tcgccaagg gggacagctc tttgccgcct ggaag           45

<210> 220
<211> 1503
<212> DNA
<213> Homo sapiens

<400> 220
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gcttctgttg ctactgaggc acggggccca ggggaagcca tcccagacg caggccctca 120
tggccagggg agggtgcacc aggcggcccc cctgagcgc gctccccatg atgacgccc 180
cgggaaacttc cagtagcacc atgaggctt cctgggacgg gaagtggcca aggaattcga 240
ccaaactcacc ccagaggaaa gccagggccg tctggggccg atcgtggacc gcatggaccg 300
cgcgggggac ggacggcgt gggtgtcgct ggccgagcgtt cgccgtgga tcgcgcacac 360
gcagcagcgg cacatacggg actcggtgag cgccgcctgg gacacgtacg acacggaccg 420
cgacggcgt gtgggttggg aggagctgctg caacgcccacc tatggccact acgcgcccgg 480
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tgcctggcct ggcctgggac acctcctctc tgccaggagg caataaaagc cagcgccggg 1440
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aaa                                         1503

<210> 221
<211> 328
<212> PRT
<213> Homo sapiens

<400> 221
Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

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Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly			
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Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala			
35	40	45	
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val			
50	55	60	
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu			
65	70	75	80
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp			
85	90	95	
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg			
100	105	110	
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp			
115	120	125	
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly			
130	135	140	
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr			
145	150	155	160
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp			
165	170	175	
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu			
180	185	190	
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr			
195	200	205	
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu			
210	215	220	
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Pro Ala			
225	230	235	240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn			
245	250	255	
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro			
260	265	270	
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu			
275	280	285	

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
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Leu Thr Arg His His Asp Glu Leu  
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<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

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20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 225  
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt 44  
  
 <210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 226  
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 ccagcctgtc tgcgtcggt ttggcgcccc cgcctcccg cggtgccgggg ttgcacacccg 180  
 atcctgggc tgcgtcgatt tgccgcccag ggcctccca gaccttagagg ggcgtggcc 240  
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 gcggggctct gaggaggtga cgcgccgggc ctccgcacc ctggccttgc cgcatttctc 360  
 cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atcccggtc 420  
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 gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtggc cttgttcaag 1020  
 ccagtgaaca tcccaaataa gaattttact taaaaaactt tacatcagcc aaagatgttt 1080  
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 aaa 2403

<210> 227

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 227

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Leu	Leu	Pro	Gly	Pro	Ala	Gly	Ser	Glu	Gly	Ala	Ala	Pro	Ile	Ala	Ile
															30
20							25								

Thr	Cys	Phe	Thr	Arg	Gly	Leu	Asp	Ile	Arg	Lys	Glu	Lys	Ala	Asp	Val
															45
35							40								

Leu	Cys	Pro	Gly	Gly	Cys	Pro	Leu	Glu	Glu	Phe	Ser	Val	Tyr	Gly	Asn
															60
50							55								

Ile	Val	Tyr	Ala	Ser	Val	Ser	Ser	Ile	Cys	Gly	Ala	Ala	Val	His	Arg
															80
65							70			75					

Gly	Val	Ile	Ser	Asn	Ser	Gly	Gly	Pro	Val	Arg	Val	Tyr	Ser	Leu	Pro
															95
85								90							

Gly	Arg	Glu	Asn	Tyr	Ser	Ser	Val	Asp	Ala	Asn	Gly	Ile	Gln	Ser	Gln
															110
100							105								

Met	Leu	Ser	Arg	Trp	Ser	Ala	Ser	Phe	Thr	Val	Thr	Lys	Gly	Lys	Ser
															125
115							120								

Ser	Thr	Gln	Glu	Ala	Thr	Gly	Gln	Ala	Val	Ser	Thr	Ala	His	Pro	Pro
															140
130							135								

Thr	Gly	Lys	Arg	Leu	Lys	Lys	Thr	Pro	Glu	Lys	Lys	Thr	Gly	Asn	Lys
															160
145					150				155						

Asp	Cys	Lys	Ala	Asp	Ile	Ala	Phe	Leu	Ile	Asp	Gly	Ser	Phe	Asn	Ile
															175
165							165		170						

Gly	Gln	Arg	Arg	Phe	Asn	Leu	Gln	Lys	Asn	Phe	Val	Gly	Lys	Val	Ala
															190
180							180		185						

Leu	Met	Leu	Gly	Ile	Gly	Thr	Glu	Gly	Pro	His	Val	Gly	Leu	Val	Gln
															205
195							200				205				

Ala	Ser	Glu	His	Pro	Lys	Ile	Glu	Phe	Tyr	Leu	Lys	Asn	Phe	Thr	Ser
															220
210						215				220					

Ala	Lys	Asp	Val	Leu	Phe	Ala	Ile	Lys	Glu	Val	Gly	Phe	Arg	Gly	Gly
															240
225					230			235							

Asn	Ser	Asn	Thr	Gly	Lys	Ala	Leu	Lys	His	Thr	Ala	Gln	Lys	Phe	Phe
															255
245							245		250			255			

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
 260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
 515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
 530 535 540

Phe Leu Glu Ser Gln Gln  
 545                            550

<210> 228  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 228  
 tggtctcgca caccgatc

18

<210> 229  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 229  
 ctgctgtcca caggggag

18

<210> 230  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 230  
 ccttgaaagca tactgctc

18

<210> 231  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 231  
 gagatagcaa ttcccgcc

18

<210> 232

<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 232		
ttcctcaaga gggcagcc		18
<210> 233		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 233		
cttggcacca atgtccgaga ttcc		24
<210> 234		
<211> 45		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 234		
gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg		45
<210> 235		
<211> 2586		
<212> DNA		
<213> Homo sapiens		
<400> 235		
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gtcggggcgg cggctgcggg cgcaagacgg agatgcagcg gcttggggcc accctgttgt 180		
gcctgtgtgt ggccggggcg gtccccacgg ccccccggcc cgctccgacg ggcacccgg 240		
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tgttccgcga ggttgaggaa ctgatggagg acacgcagca caaatgcgc agcgcgggtgg 360		
aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaact 420		
tacctcccaag ctatcacaat gagaccaaca cagacacgaa ggttggaaat aataccatcc 480		
atgtgcaccc agaaattcac aagataacca acaaccagac tggacaaatg gtctttcag 540		
agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcacatcg 600		
acgaggactg tggggccagc atgtactgcc agtttgcacg cttoccagtc acctgcccagc 660		
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<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala  
1 5 10 15

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val  
20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
                  35                 40                 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
                   85                     90                     95  
  
 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
                   100                    105                    110  
  
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
                   115                    120                    125  
  
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
                   130                    135                    140  
  
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
                   145                    150                    155                    160  
  
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
                   165                    170                    175  
  
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
                   180                    185                    190  
  
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
                   195                    200                    205  
  
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
                   210                    215                    220  
  
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
                   225                    230                    235                    240  
  
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
                   245                    250                    255  
  
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
                   260                    265                    270  
  
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
                   275                    280                    285  
  
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
                   290                    295                    300  
  
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
                   305                    310                    315                    320  
  
 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
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 Pro Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
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<211> 17		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic oligonucleotide probe		
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&lt;211&gt; 713

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 245

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Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
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Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
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 Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu  
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 Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn  
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 Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn  
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 Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys  
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 395 400 405  
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Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val		
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Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu		
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Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His		
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Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr		
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Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr		
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<212> DNA

<213> Homo Sapien

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 35 40 45  
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 50 55 60  
 Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr  
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 80 85 90  
 Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

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Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
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Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
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Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
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Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
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Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
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Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr		
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Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser		
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<212> DNA

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<223> Synthetic Oligonucleotide Probe

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<210> 252

<211> 24

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<220>  
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aagtgcact ttgcgggggt tgccttgggt gattcctgga tctccccgt 650  
tgattcggtg ctctcctggg gaccttacct gtacagcatg tctttctcg 700



Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn  
 50 55 60  
 Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln  
 65 70 75  
 Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu  
 80 85 90  
 Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp  
 95 100 105  
 Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr  
 110 115 120  
 Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu  
 125 130 135  
 Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe  
 140 145 150  
 Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser  
 155 160 165  
 Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu  
 170 175 180  
 Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly  
 185 190 195  
 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu  
 200 205 210  
 Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys  
 215 220 225  
 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala  
 230 235 240  
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys  
 245 250 255  
 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr  
 260 265 270  
 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser  
 275 280 285  
 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His  
 290 295 300  
 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp		
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe		
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly		
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp		
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu		
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp		
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn		
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser		
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln		
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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tgctgctggc tcgggctgga ctcaggaagc cggagtgcgc ggaggcggcg 100

ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcacgtggg 150

tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtggattc ccacgtatgc ggagtgcgc tgctcagcca ccgctggca 250

ctcacggcgg cgcaactgctt tgaaacctat agtgcacctta gtgatccctc 300

cgggtggatg gtccagtttgc cccagctgac ttccatgcca tccttctgga 350

gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

cctcgctacc tgggaaattc accctatgac attgccttgg tgaagctgtc 450  
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tggggccggc ctgagcctac ctgagccccat gcagcctggg gccactgcca 1000  
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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg  
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Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser

20                          25                          30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly  
35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg  
50 55 60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg  
65 70 75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu  
80 85 90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
                   95                     100                     105  
  
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
                   110                    115                     120  
  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
                   125                    130                     135  
  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
                   140                    145                     150  
  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
                   155                    160                     165  
  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
                   170                    175                     180  
  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
                   185                    190                     195  
  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
                   200                    205                     210  
  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
                   215                    220                     225  
  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
                   230                    235                     240  
  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
                   245                    250                     255  
  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
                   260                    265                     270  
  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
                   275                    280                     285  
  
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu  
                   290                    295                     300  
  
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val  
                   305                    310

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

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cgaggccccga ccagcggagg acgctgcccc caggctgggt gtccctgggc 150  
cgtgcggacc ctgaggaaga gctgagtctc acctttgccccc tgagacagca 200  
gaatgtggaa agactctcg agctggtgca ggctgtgtcg gatcccagct 250  
ctcctcaata cgaaaaatac ctgaccctag agaatgtggc tgatctggtg 300  
aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350  
cgagccccag aagtgcatt ctgtgatcac acaggacttt ctgacttgct 400  
ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagttcat 450  
caatatgtgg gaggacctac ggaaacccat gttgtaaggt ccccacatcc 500  
ctaccagctt ccacaggcct tggcccccca tgtggacttt gtggggggac 550  
tgcaccgttt tcccccaaca tcataccctga ggcaacgtcc tgagccgcag 600  
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tgagctatgg agatgatgag gactccctca gcagcgccta catccagcgg 1050  
gtcaacactg agctcatgaa ggctgcccgt cggggctctca ccctgctctt 1100  
cgccctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150  
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ggcacatcct tccaggaacc tttcctcatc acaaatgaaa ttgttgacta 1250  
tatcagtgggt ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300  
aggaagctgt aacgaagttc ctgagctcta gcccccacct gccaccatcc 1350  
agttacttca atgcccagtgg ccgtgcctac ccagatgtgg ctgcactttc 1400

tgatggctac tgggtggtca gcaacagagt gcccattcca tgggtgtccg 1450  
 gaacctcgcc ctctactcca gtgttgggg ggatcctatc cttgatcaat 1500  
 gagcacagga tccttagtgg ccgcggccct cttggcttc tcaacccaag 1550  
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 agccctgctg aaccctcaac tattgactgc tgcagacagc ttatctccct 1850  
 aaccctgaaa tgctgtgagc ttgacttgac tcccaaccct accatgatcc 1900  
 atcatactca ggtctcccta ctcctgcctt agattcctca ataagatgct 1950  
 gtaactagca tttttgaat gcctctccct ccgcattctca tctttctt 2000  
 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050  
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 tttactctt cctaccctga catccagaaa caatggcctc cagtcatac 2150  
 ttctcaatct ttgctttatg gccttccat catagttgcc cactccctt 2200  
 ctttacttag cttccaggc ttaacttctc tgactactt tgtcttcctc 2250  
 tctcatcaat ttctgcttct tcatggaatg ctgacccatca ttgctccatt 2300  
 tgttagattt tgctcttctc agtttactca ttgtccctg gaacaaatca 2350  
 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400  
 aatgattgat acctcaaatg taaaaaa 2427

<210> 259  
 <211> 556  
 <212> PRT  
 <213> Homo Sapien

<400> 259  
 Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu  
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Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

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Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu		
35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly
				290					295					300
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser
				305					310					315
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp
				320					325					330
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met
				335					340					345
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp
				350					355					360
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg
				365					370					375
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly
				380					385					390
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp
				395					400					405
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser
				410					415					420
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His
				425					430					435
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro
				440					445					450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg
				455					460					465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val
				470					475					480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser
				485					490					495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln
				500					505					510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser
				515					520					525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro
				530					535					540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu
				545					550					555

## Cys

<210> 260  
 <211> 1638  
 <212> DNA  
 <213> Homo Sapien

<400> 260  
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 attccagggc tcctcttcat tctttttttt ctgtctgtg ctgttggca 150  
 agtgagccct tacagtgcacc cctggaaacc cacttggcct gcataccgcc 200  
 tccctgtcggt cttgccccag tctaccctca attttagccaa gccagacttt 250  
 ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300  
 taaggaaact ccactgcccc cttacgaaga ggccaagcaa tatctgtctt 350  
 atgaaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcattc 400  
 tacatcctca gcagtagtggtt agatggggcc caacaccggag actcagggtc 450  
 ttcagggaaag tctcgaaggaa agcggcagat ttatggctat gacagcagg 500  
 tcagcatttt tgggaaggac ttccctgctca actacccttt ctcaacatca 550  
 gtgaagttat ccacgggctg caccggcacc ctgggtggcag agaagcatgt 600  
 cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 650  
 cccagaagct tcgagtgggc ttccctaaagc ccaagttaa agatgggttgt 700  
 cgagggggcca acgactccac ttccatggcattt cccgagcaga tgaaatttca 750  
 gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaaggcga 800  
 atgccaatga catcggtatg gattatgatt atgcccctctt ggaactcaaa 850  
 aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctccctgctaa 900  
 gcagctgcca gggggcagaa ttccatgttc tggttatgac aatgaccgac 950  
 caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000  
 ttgctctacc agcaatgcga tgcccgccaa gggggccagcg ggtctgggt 1050  
 ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100

ttggcattt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
gatttcaacg tggctgtcag aatcactctt ctcaaataatg cccagatttg 1200  
ctattggatt aaaggaaact acctggattt tagggagggg tgacacagtg 1250  
ttccctcctg gcagcaatta agggtcttca tgttcttatt ttaggagagg 1300  
ccaaattgtt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
tgtgtgttaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400  
tgactggctt tactatttga aaactggttt gtgtatcata tcataatatca 1450  
tttaagcagt ttgaaggcat acttttgcatt agaaataaaaa aaaataactga 1500  
tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgttttg 1550  
caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600  
atattggca tacaagagat atgaaaaaaaaaaa 1638

<210> 261  
<211> 383  
<212> PRT  
<213> Homo Sapien



<210> 262  
<211> 1378  
<212> DNA  
<213> Homo Sapien

<400> 262  
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ccatgggtt ttctggagcg ccccccagcccc tgggtggggg ctgtctcgcc 100  
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caggataacctt gttccccccag cctgtggaa gccccagcag ctgaaccggg 200  
tttgtggcgcc cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
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ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350  
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
cggtcccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450  
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aataggctca tctacactcta cctctggggg cccggacggc tgctgcggaa 1150

aggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200  
catcaggccc cgcccaacgg cctcatgtcc ccgcccccac gacttccggc 1250  
cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300  
ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350  
ataaaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu
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Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
					20					25				30
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
					35					40				45
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
					50					55				60
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
					65					70				75
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
					80					85				90
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
					95					100				105
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
					110					115				120
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
					125					130				135
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
					140					145				150
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
					155					160				165
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp
					170					175				180

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu  
                   185                     190                 195  
 Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His  
                   200                     205                 210  
 Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met  
                   215                     220                 225  
 Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly  
                   230                     235                 240  
 Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu  
                   245                     250                 255  
 Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn  
                   260                     265                 270  
 Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val  
                   275                     280                 285  
 Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly  
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 Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala  
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 <400> 265  
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 <210> 266  
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<220>  
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<400> 266  
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<210> 267  
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<220>  
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<400> 267  
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<210> 268  
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<400> 268  
ggggaaattca ccctatgaca ttgcc 25

<210> 269  
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<400> 269  
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<210> 270  
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<220>  
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<400> 270  
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<210> 271  
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<400> 271  
gcggaaggc agaatggac tccaaag 26

<210> 272  
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<220>  
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<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
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<400> 273  
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<210> 274  
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<210> 277  
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<400> 277  
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<210> 278  
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<400> 278  
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<210> 279  
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<400> 279  
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<210> 280  
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<212> DNA  
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<210> 281

<211> 34

<212> DNA

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<400> 281  
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<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

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tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

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gcagccatct gtactggcg ggagcaggac agggaccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gtttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgttga tggtgagct gcacaacctc taccggggccc 150  
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250  
 caaggagcgc gggcgccgag gcgagaatct gttcgccatc acagacgagg 300  
 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350  
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 cacgcaggtg gtagggcca agacagagag gatcggctgt ggttcccact 450  
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 aatgggtact ctttcttccc tagcaacggg gattccggct ttcttggtaa 750  
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ataaaaaacct gtccaaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu
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Leu Leu Leu Val Ala Thr Thr Gly Pro Val Gly Ala Leu Thr Asp  
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Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala  
35 40 45

Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp  
50 55 60

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val  
65 70 75

Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe  
80 85 90

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu  
95 100 105

Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys  
110 115 120

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala  
125 130 135



Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
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<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagg ttccatgtgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

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caaggcaagt tccatgagcc accttcaaag cttcgagaa gtgaaaactga 200  
acaacaatga attggagacc attccaaatc tggaccagt ctggcaaat 250  
attacacttc tctccttggc tggaaacagg attgttggaaa tactccctga 300  
acatctgaaa gagttcagt ccctgaaac tttggacctt agcagcaaca 350  
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 <211> 1059  
 <212> PRT  
 <213> Homo Sapien

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Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
                   35                        40                        45  
 Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
                   50                        55                        60  
 Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
                   65                        70                        75  
 Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
                   80                        85                        90  
 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
                   95                        100                      105  
 Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
                   110                      115                      120  
 Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
                   125                      130                      135  
 Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
                   140                      145                      150  
 Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn  
                   155                      160                      165  
 Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala  
                   170                      175                      180  
 Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met  
                   185                      190                      195  
 Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu  
                   200                      205                      210  
 Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly  
                   215                      220                      225  
 Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn  
                   230                      235                      240  
 Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu  
                   245                      250                      255  
 Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser  
                   260                      265                      270  
 Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn  
                   275                      280                      285  
 Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser

290	295	300
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Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg 320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala 335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn 350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys 365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys 380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln 395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly 410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp 425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala 440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser 455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu 470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln 485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu 500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn 515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn 530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg 545	550	555

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro  
                   560                     565                 570  
  
 Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro  
                   575                     580                 585  
  
 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val  
                   590                     595                 600  
  
 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser  
                   605                     610                 615  
  
 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr  
                   620                     625                 630  
  
 Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp  
                   635                     640                 645  
  
 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala  
                   650                     655                 660  
  
 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser  
                   665                     670                 675  
  
 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln  
                   680                     685                 690  
  
 Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr  
                   695                     700                 705  
  
 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val  
                   710                     715                 720  
  
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met  
                   725                     730                 735  
  
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val  
                   740                     745                 750  
  
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val  
                   755                     760                 765  
  
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Asn Glu Asp Cys  
                   770                     775                 780  
  
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
                   785                     790                 795  
  
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
                   800                     805                 810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 815 820 825  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 845 850 855  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
 860 865 870  
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 890 895 900  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
 905 910 915  
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
 920 925 930  
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 935 940 945  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
 950 955 960  
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
 965 970 975  
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
 980 985 990  
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
 995 1000 1005  
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
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 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
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 Asn Phe Gln Ser Tyr Asp Leu Asp Thr  
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&lt;211&gt; 2906

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

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<400> 292

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Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
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Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
														60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
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Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
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Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
														105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
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Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
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Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
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Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

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Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly		
185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg		
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Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp		
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Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln		
230	235	240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile		
245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val		
260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp		
275	280	285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His		
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Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp		
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Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro		
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Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn		
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Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val		
395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp		
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 Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
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 Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
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Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met		
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Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu		
260	265	270
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly		
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Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn		
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Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
335	340	345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		
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Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
365	370	375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
380	385	390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
395	400	405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
410	415	420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
425	430	435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
440	445	450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
455	460	465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
470	475	480



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 770 775 780  
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met  
 785 790 795  
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val  
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 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val  
 815 820 825  
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys  
 830 835 840  
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
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 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
 860 865 870  
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 875 880 885  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 890 895 900  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
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 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 950 955 960  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
 965 970 975  
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
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 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
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&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 295

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&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

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&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

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<210> 308  
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<210> 309  
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<210> 310  
<211> 3296  
<212> DNA  
<213> Homo Sapien

<400> 310

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<210> 312  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 312  
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<210> 313  
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<220>  
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<400> 313  
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<210> 314  
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<212> DNA  
<213> Homo Sapien

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&lt;210&gt; 315

&lt;211&gt; 509

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

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Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys			
35	40	45	
Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys			
50	55	60	
Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys			
65	70	75	
Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu			
80	85	90	
Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met			
95	100	105	
Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met			
110	115	120	
Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met			
125	130	135	
Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg			
140	145	150	
Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg			
155	160	165	

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys  
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 Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys  
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 Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr  
                   200                     205                  210  
  
 Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys  
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 Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys  
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 Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr  
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 Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn  
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                   350                     355                  360  
  
 Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln  
                   365                     370                  375  
  
 Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val  
                   380                     385                  390  
  
 His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu  
                   395                     400                  405  
  
 Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly  
                                      410                     415                  420  
  
 Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys

425                    430                    435

Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly  
440                    445                    450

Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser  
455                    460                    465

Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala  
470                    475                    480

Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln  
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<223> Synthetic Oligonucleotide Probe

<400> 317  
ttgcacttgt aggacccacg tacg 24

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<223> Synthetic Oligonucleotide Probe

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<210> 319  
<211> 2110  
<212> DNA

<213> Homo Sapien

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Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe			
35	40	45	
His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg			
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Pro	His	Thr	Met	Pro	Lys	Tyr	Leu	Leu	Gly	Ser	Val	Asn	Lys	Ser
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Val	Val	Pro	Asp	Leu	Glu	Tyr	Gln	His	Lys	Phe	Thr	Met	Met	Pro
				80					85				90	
Pro	Asn	Ala	Ser	Leu	Leu	Ile	Asn	Pro	Leu	Gln	Phe	Pro	Asp	Glu
				95					100				105	
Gly	Asn	Tyr	Ile	Val	Lys	Val	Asn	Ile	Gln	Gly	Asn	Gly	Thr	Leu
				110					115				120	
Ser	Ala	Ser	Gln	Lys	Ile	Gln	Val	Thr	Val	Asp	Asp	Pro	Val	Thr
				125					130				135	
Lys	Pro	Val	Val	Gln	Ile	His	Pro	Pro	Ser	Gly	Ala	Val	Glu	Tyr
				140					145				150	
Val	Gly	Asn	Met	Thr	Leu	Thr	Cys	His	Val	Glu	Gly	Gly	Thr	Arg
				155					160				165	
Leu	Ala	Tyr	Gln	Trp	Leu	Lys	Asn	Gly	Arg	Pro	Val	His	Thr	Ser
				170					175				180	
Ser	Thr	Tyr	Ser	Phe	Ser	Pro	Gln	Asn	Asn	Thr	Leu	His	Ile	Ala
				185					190				195	
Pro	Val	Thr	Lys	Glu	Asp	Ile	Gly	Asn	Tyr	Ser	Cys	Leu	Val	Arg
				200					205				210	
Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile
				215					220				225	
Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu
				230					235				240	
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu
				245					250				255	
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp
				260					265				270	
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro
				275					280				285	
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp
				290					295				300	
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu
				305					310				315	
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
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Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu		
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

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<210> 322  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 322  
cactgacagg gttcctcacc cagg 24

<210> 323  
<211> 45  
<212> DNA  
<213> Artificial Sequence

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&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 323

ctccctctgg gctgtggagt atgtgggaa catgaccctg acatg 45

&lt;210&gt; 324

&lt;211&gt; 2397

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 324

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cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100

acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aattttatgc cccgtggtgc cctgcttgc aaaatcttca 200

accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250

ttcgaaaagt agatgtcaca gagcagccag gactgagtgg acggttatac 300

ataactgctc ttcctactat ttatcattgt aaagatggtg aatttaggcg 350

ctatcagggc ccaaggacta agaaggactt cataaacttt ataagtgata 400

aagagtggaa gagtatttag cccgtttcat catggtttg tccaggtct 450

gttctgatga gtagtatgtc agcactctt cagctatcta tgtggatcag 500

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<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

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20

25

30

Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly

35

40

45

Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln

50

55

60

Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp

65

70

75

Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly

80

85

90

Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His

95

100

105

Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys

110

115

120

Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile

125

130

135

Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser

140

145

150

Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys

155

160

165

His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser

170

175

180

Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu

185

190

195

Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	Ser	Lys

200

205

210

Arg Arg Arg Pro Gln Pro Tyr Pro Ser Lys Lys Leu Leu

215 220 225

Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu  
230 235 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu  
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<210> 326  
<211> 23  
<212> DNA

<213> Artificial Sequence

<220>  
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tgaggtggc aagcggcgaa atg 23

<210> 327  
<211> 20  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 327  
tatgtggatc aggacgtgcc 20

<210> 328  
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<223> Synthetic Oligonucleotide Probe

<400> 328  
tgcagggttc agtcttagatt g 21

<210> 329  
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<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 329  
ttgaaggaca aaggcaatct gccac 25  
  
<210> 330  
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<223> Synthetic Oligonucleotide Probe  
  
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<210> 331  
<211> 2168  
<212> DNA  
<213> Homo Sapien  
  
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<210> 332  
 <211> 533  
 <212> PRT  
 <213> Homo Sapien

<400> 332  
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       20                   25                     30

Thr Asp Leu Ile Tyr Ala Glu Glu Leu Val Gln Ser Leu Lys  
       35                   40                     45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser  
       50                   55                     60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp  
       65                   70                     75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val  
       80                   85                     90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu  
       95                   100                    105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg  
       110                  115                    120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala  
       125                  130                    135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile  
       140                  145                    150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser  
       155                  160                    165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly  
       170                  175                    180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln  
       185                  190                    195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Lys Ser Gln Val Leu  
       200                  205                    210

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg  
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 Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His  
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 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu  
                  245                     250                     255  
  
 Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu  
                  260                     265                     270  
  
 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro  
                  275                     280                     285  
  
 Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys  
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 Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His  
                  305                     310                     315  
  
 Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu  
                  320                     325                     330  
  
 Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met  
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 Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys  
                  350                     355                     360  
  
 Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr  
                  365                     370                     375  
  
 Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp  
                  380                     385                     390  
  
 Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile  
                  395                     400                     405  
  
 Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn  
                  410                     415                     420  
  
 Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg  
                  425                     430                     435  
  
 Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala  
                  440                     445                     450  
  
 Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr  
                  455                     460                     465  
  
 Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr  
                  470                     475                     480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
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Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp  
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<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 333

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<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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<400> 336
acactcagca ttgcctggta ct tg 24

<210> 337
<211> 45
<212> DNA
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<220>
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<400> 337
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<210> 338
<211> 2789

<212> DNA
<213> Homo Sapien

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gggcacccggc gggccctggc tcgcagggtc agcctgtgc gcccactgag 1750  
ccgggtggaa atccctaccta tgccctatgt cactgaggcc acccgagtgc 1800  
agctggtgct gccactcctg gtggctgaag ctgctgcagc cccggcttcc 1850  
ctcgaggcgt ttgcagccaa tgtcctggag ccacgagaac atgcattgt 1900  
caccctgttg ctggtctacg ggcacgaga aggtggccgt ggagctccag 1950  
accacatttct tgggtgtgaag gctgcagcag cggagttaga gcgacggta 2000  
cctgggacga ggctggcctg gctcgctgtg cgagcagagg ccccttccca 2050  
ggtgcgactc atggacgtgg tctcgaagaa gcaccctgtg gacactctct 2100

tcttccttac caccgtgtgg acaaggcctg gggccgaagt cctcaaccgc 2150  
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ccaggagttc aatcctgccc tgtcaccaca gagatcaccc ccagggcccc 2250  
cgggggctgg ccctgacccc ccctccctc ctggtgctga cccctcccg 2300  
ggggctccta taggggggag atttgaccgg caggcttctg cggagggctg 2350  
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tggcaggcca ggaagaggag gaagccctgg aggggctgga ggtgatggat 2450  
gttttctcc ggttctcagg gctccacctc tttagggccg tagagccagg 2500  
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gcccgcctgg gggccctaac ctcattacct ttcccttgtc tgccctcagcc 2700  
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tttttaata taaaaatgtt attaaacatg tttctgcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met Arg Leu Ser Ser Leu Leu Ala Leu Leu Arg Pro Ala Leu Pro  
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Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg  
20 25 30

Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala  
35 40 45

Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg  
50 55 60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr  
65 70 75

Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg  
80 85 90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser	Thr Leu Ala Val Ala Val	
110	115	120
Asn Arg Thr Val Ala His His Phe Pro Arg	Leu Leu Tyr Phe Thr	
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met	Gln Val Val Ser	
140	145	150
His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser	Glu Thr Leu Arg	
155	160	165
His Leu His Thr His Phe Gly Ala Asp Tyr Asp	Trp Phe Phe Ile	
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg	Leu Ala Ala Leu	
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp	Leu Tyr Leu Gly Arg Ala	
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg	Tyr Cys His Gly	
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser	Leu Leu Leu Arg Leu Arg	
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp	Ile Leu Ser Ala Arg Pro	
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp	Ser Leu Gly Val Gly	
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln	Tyr Arg Ser Phe Glu Leu	
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser	Ser Ala Phe Leu	
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser	Glu Gly Thr Leu Met Tyr	
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu	Glu Arg Ala Tyr	
320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile	Arg Asn Leu Thr Val	
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp	Pro Val Gly Leu	
350	355	360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp  
                   365                  370                  375  
  
 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala  
                   380                  385                  390  
  
 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp  
                   395                  400                  405  
  
 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro  
                   410                  415                  420  
  
 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg  
                   425                  430                  435  
  
 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu  
                   440                  445                  450  
  
 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg  
                   455                  460                  465  
  
 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met  
                   470                  475                  480  
  
 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu  
                   485                  490                  495  
  
 Leu Val Ala Glu Ala Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe  
                   500                  505                  510  
  
 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu  
                   515                  520                  525  
  
 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp  
                   530                  535                  540  
  
 Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg  
                   545                  550                  555  
  
 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala  
                   560                  565                  570  
  
 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro  
                   575                  580                  585  
  
 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly  
                   590                  595                  600  
  
 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp  
                   605                  610                  615  
  
 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu  
                   620                  625                  630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
                   635                       640                  645  
  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
                   650                       655                  660  
  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
                   665                       670                  675  
  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
                   680                       685                  690  
  
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
                   695                       700                  705  
  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
                   710                       715                  720  
  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
                   725                       730                  735  
  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
                   740                       745                  750  
  
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
                   755                       760                  765  
  
 Gln Glu Gln Ala Asn Ser Thr  
                   770

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 <211> 1572  
 <212> DNA  
 <213> Homo Sapien

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 ctttttgaag ggtgtatgc ttggaagcat tttctgtgct ttgatcacta 150  
  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
  
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
  
 ggtatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
  
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350  
  
 accaaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gttttagtca attaatatgg acacaaatga catgtggta atgatgagaa 450  
 aagcttacaa atacgcctt gataagtata gagaccaata caactggtc 500  
 ttccttgcac gccccactac gtttgctatc attgaaaacc taaagtattt 550  
 tttgttaaaa aaggatccat cacagcctt ctatctaggc cacactataa 600  
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700  
 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
 cagttgcct gaaatatgct ggagtatttgc cagaaaatgc agaagatgct 800  
 gatggaaaag atgtatttaa taccaaatact gttggcctt ctattaaaga 850  
 ggcaatgact tatcacccca accaggttgt agaaggctgt tgccagata 900  
 tggctgttac tttaatgga ctgactccaa atcagatgca tgtgatgatg 950  
 tatgggttat accgccttag ggcatttggg catatttca atgatgcatt 1000  
 ggtttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050  
 agcgtgaata tgatcttgc ataggacgtg tgccgtcatt atttgcatt 1100  
 gtaactacat atccaataaca gctgtatgtt tcttttctt ttctaatttgc 1150  
 gtggcactgg tataaccaca cattaaagtc agtagtacat tttaatgaa 1200  
 gggtggtttt ttctttaaa acacatgaac attgtaaatg tgccggaaag 1250  
 aagtgttttta agaataataa ttttgcacaa aaactattaa taaatattat 1300  
 atgtgataaa ttctaaatata tgaacattag aaatctgtgg ggacacatatt 1350  
 tttgctgatt gttaaaaaaa tttaacagg tctttgcgt tctaagat 1400  
 gcaaatgata tctctagttg tgaatttgcgt attaaagtaa aacttttagc 1450  
 tgtgtgttcc cttaacttct aatactgatt tatgttctaa gcctccccaa 1500  
 gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaaa 1550  
 attaaagtga aagttgaaaa at 1572

<210> 341  
 <211> 318  
 <212> PRT  
 <213> Homo Sapien

&lt;400&gt; 341

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Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile
					20				25					30
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	Leu	Gln	
					35				40					45
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
					50				55					60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
					65				70					75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
					80				85					90
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
					95				100					105
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
					110				115					120
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
					125				130					135
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
					140				145					150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
					155				160					165
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
					170				175					180
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
						185			190					195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
						200			205					210
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
					215				220					225
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
					230				235					240
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
					245				250					255
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

260                    265                    270  
Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln  
                      275                        280                        285  
Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly  
                      290                        295                        300  
His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser  
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Asp Asn Asp

<210> 342  
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<220>  
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<212> DNA  
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ctgggttcttc cttgcacg 18  
  
<210> 344  
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<212> DNA  
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<210> 345  
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<223> Synthetic Oligonucleotide Probe  
  
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<210> 346  
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<212> DNA  
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gggatgcagg tggtgtctca tgggg 25  
  
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<211> 18  
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<223> Synthetic Oligonucleotide Probe  
  
<400> 347  
ccctcatgta ccggctcc 18  
  
<210> 348  
<211> 48  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 348  
ggattctaat acgactcaact atagggtctca gaaaagcgca acagagaa 48  
  
<210> 349  
<211> 47  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 349  
ctatgaaatt aaccctcaact aaagggatgt cttccatgcc aaccttc 47  
  
<210> 350  
<211> 48  
<212> DNA  
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<220>  
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<210> 351  
<211> 48  
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<220>  
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<400> 351  
ctatgaaatt aaccctcact aaagggacga ggaagatggg cggatgg 48  
  
<210> 352  
<211> 47  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
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<211> 48  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 353  
ctatgaaatt aaccctcact aaagggacgg gggacaccac ggaccaga 48  
  
<210> 354  
<211> 48  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 354  
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<210> 355  
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<212> DNA  
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<220>  
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<400> 355  
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<210> 356  
<211> 46  
<212> DNA  
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<220>  
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<400> 356  
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<210> 357  
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<220>  
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<400> 357  
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<210> 358  
<211> 47  
<212> DNA  
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<220>  
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<400> 358  
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<210> 359  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 359  
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<210> 360  
<211> 48  
<212> DNA  
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<220>  
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<400> 360  
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<210> 361  
<211> 48  
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<400> 361  
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<210> 362  
<211> 47  
<212> DNA  
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<220>  
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<400> 362  
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<210> 363  
<211> 48  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 363  
ctatgaaatt aaccctcaact aaagggagga ttgcacggac cttcacag 48

<210> 364  
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<212> DNA  
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<400> 364

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<210> 365  
<211> 48  
<212> DNA  
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<220>  
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<210> 366  
<211> 48  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 366  
ggattctaat acgactcact atagggcgca gcgatggcag cgatgagg 48  
  
<210> 367  
<211> 47  
  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 367  
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<210> 368  
<211> 47  
<212> DNA  
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<220>  
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<400> 368  
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<210> 369  
<211> 48  
<212> DNA  
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<220>

<223> Synthetic Oligonucleotide Probe

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<210> 370  
<211> 48  
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<220>

<223> Synthetic Oligonucleotide Probe

<400> 370  
ggattctaat acgactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371  
<211> 48  
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<220>

<223> Synthetic Oligonucleotide Probe

<400> 371  
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<210> 372  
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<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372  
ggattctaat acgactcact atagggccag ggaaatccgg atgtctc 47

<210> 373  
<211> 48  
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<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373  
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<210> 374  
<211> 47  
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<400> 374  
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<210> 375  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 375  
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<210> 376  
<211> 997  
<212> DNA  
<213> Homo Sapien

<400> 376  
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tgcttccttt cccaaatgtt cttatggact gttgctggga tccccatcct 200  
atttctcagt gcctgtttca tcaccagatg ttttgtgaca tttcgcatct 250  
ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300  
ctctcctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350  
gaactggaa tattttcaat ccagctgcta cttctttct actgacacca 400  
tttcctgggc gttaagttt aagaactgct cagccatggg ggctcacctg 450  
gtggttatca actcacagga ggagcaggaa ttcccttcct acaagaaaacc 500  
taaaatgaga gagttttta ttggactgtc agaccagggtt gtcgagggtc 550  
agtggcaatg ggtggacggc acaccttga caaagtctct gagttctgg 600  
gatgttaggg agcccaacaa catagctacc ctggaggact gtgccaccat 650  
gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700  
tcaatttattt tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750

ggaaaatctc tttaagaaca gaaggcacaa ctcaaatgtg taaagaagga 800  
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850  
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900  
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 997

&lt;210&gt; 377

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 377

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Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro	
					20				25				30		
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr	
					35				40				45		
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro	
					50				55				60		
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser	
					65				70				75		
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser	
					80				85				90		
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu	
					95				100				105		
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser	
					110				115				120		
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	
					125				130				135		
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp	
					140				145				150		
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp	
					155				160				165		
Asp	Val	Gly	Glu	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala
					170				175				180		

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
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Asn Pro Leu Asn Lys Gly Lys Ser Leu  
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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<210> 380

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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gggactgaac tgccagcttc 20

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&lt;210&gt; 423

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 423

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Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu			
35	40		45
Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr			
50	55		60
Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr			
65	70		75
Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly			
80	85		90
Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val			
95	100		105
Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg			
110	115		120
Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val			
125	130		135
Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val			
140	145		150
Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly			
155	160		165
His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu			
170	175		180
Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe			
185	190		195

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His  
200 205 210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala  
215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu  
230 235 240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val  
245 250 255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly  
260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro  
275 280 285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly  
290 295 300

Asp Phe Arg His Lys Ser Ser Phe Val Ile  
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